

## SEQUENCE LISTING

<110> OULMOUDEN, AHMAD  
JULIEN, RAYMOND  
LAFORET, MARIE-PIERRE  
LEVEZIEL, HUBERT

<120> USE OF SILVER GENE FOR THE AUTHENTICATION OF  
THE RACIAL ORIGIN OF ANIMAL POPULATIONS, AND  
OF THE DERIVATIVE PRODUCTS THEREOF

<130> 0508-1156

<140> 10/565,646  
<141> 2006-03-24

<150> PCT/FR2004/001952  
<151> 2004-07-22

<150> FR/09161  
<151> 2003-07-25

<160> 18

<170> PatentIn version 3.1

<210> 1  
<211> 8146  
<212> DNA  
<213> Bos taurus

<220>  
<221> CDS  
<222> (30)..(104)  
<223> First CDS region

<220>  
<221> CDS  
<222> (2326)..(2435)  
<223> Second CDS region

<220>  
<221> CDS  
<222> (2582)..(2727)  
<223> Third CDS region

<220>  
<221> CDS  
<222> (3804)..(3937)  
<223> Fourth CDS region

<220>  
<221> CDS  
<222> (4315)..(4475)  
<223> Fifth CDS region

<220>  
<221> CDS  
<222> (4733)..(5412)  
<223> Sixth CDS region

<220>  
<221> CDS

<222> (6321)..(6436)  
 <223> Seventh CDS region

<220>  
 <221> CDS  
 <222> (6681)..(6765)  
 <223> Eighth CDS region

<220>  
 <221> CDS  
 <222> (6876)..(7080)  
 <223> Ninth CDS region

<220>  
 <221> CDS  
 <222> (7188)..(7275)  
 <223> Tenth CDS region

<220>  
 <221> CDS  
 <222> (7899)..(8036)  
 <223> Eleventh CDS region

<400> 1  
 ggtcttttggg tgctggaagg aagaacagg atg gat ctg gtg ctg aga aaa tac 53  
 Met Asp Leu Val Leu Arg Lys Tyr  
 1 5

ctt ctc cat gtg gct ctg atg ggt gtt ctt ctg gct gta ggg acc aca 101  
 Leu Leu His Val Ala Leu Met Gly Val Leu Leu Ala Val Gly Thr Thr  
 10 15 20

gaa g gtgagtgtgg gatgttggac atgaacaagt gtgaatttgg gggtgcacac 155  
 Glu  
 25

ctgctctggg	ttttctctcc	ctaaaatgga	agatatcagt	agtgccttcag	gtgtctccca	215
cccatgtgat	ttagttagga	catgggcaac	tgagctccct	ccccacatga	agatttgggt	275
gcatgtgtgt	tcaggcactt	gggactgaac	ctgaaaacaa	ccccatctac	ctggatgggt	335
gagagaacag	tatgtctccg	tggcccta	tttgagatgc	tctgaatagt	gagctggaac	395
atgggtgcca	aggtagtaaa	atgagtggaa	actcatttag	gctttgtctc	aggcacttgg	455
gatagggtat	ttaggagata	gagaaagata	ggagatagga	gaaaggagaa	agaggatgtg	515
gtattggata	gaagggtaat	gaggcacctc	atccccctct	tgggatgggc	atgggtgaac	575
acagcccagg	cttttgttct	ggggctggaa	gagacaggca	gaagggtctc	agctgagcat	635
cacatgaaag	ggctctgggg	gattggggcc	tcgtgacagg	agcaaggcgg	gtgggggtgg	695
gatggtgaga	gggtctggaa	tgtcccggtc	tgctctgagg	agggaggatt	gggagtggag	755
aaagaatggg	gcattcttat	attctcttgt	tcttgtggtg	aggtattcag	tgggataatt	815
ctagatcctc	ccccaaagaa	atcaaccagg	tttctggtac	atgttagaga	tggagtggag	875
atagtctgtg	atgtgcagaa	atatctacat	tgtaccccag	tgcccccttt	ctctagatcc	935
ctggtctcac	agacttcttg	gaacttctcc	ttgatctgac	ttccctcatt	catggtgtca	995
tttcaagtct	tattctttta	ctatgttcgt	tattgtattc	tggaaatata	ctgttcatat	1055
gtgtccaccc	aaggctctta	atatgttgtg	cttacttttt	ggatccagat	ttttaaaatc	1115
ataagaagac	atttttatat	agttcatgaa	attttgcatt	gactgagttt	gataattttg	1175
tttagtgtga	attaacattg	tgtttattta	agaaaaaaaa	atattttttt	acagaaacct	1235
actgaatttg	tagggtttta	aaataacatg	atgtctggga	tttgcttttg	aatgcttcag	1295
ccaaaaaaca	aacgaacaac	aaaaataaag	gatagataaa	gcaaagtgtg	caaaatgctg	1355
atagttgttg	gaccttgggg	agacacatgc	atagaccatca	catcactttt	tttcagacat	1415
ctttcttggg	cagttataat	cattttgttt	gtccccactc	ccaattttcta	cttgccctcta	1475
gtccatcctc	ctcactgctt	gccaaagtga	tccttctaaa	acacaaatct	gatcatattc	1535
aaaaagcttt	tgaagggtaa	gttttatggt	atatgccata	tatcagtaca	acaaacaaaa	1595
tcgtctgagg	tgccgttggc	tacaggataa	agtccaaact	cctttgcctg	gcaactcaag	1655
ccccactct	atcttcttgg	cctcatctct	catgatgtac	atcagccaca	ttgctagtgt	1715
ctgctcatgg	ccttctgcct	agaatgcttt	atgccccagc	caactattta	ctgtcttctt	1775

SEQCRF05081156

cagtcgacca	gagtgcaatt	tacctgttta	aaatctatca	ttttgttata	cattgtgcat	1835
gtctattatg	gctcatatta	agcaatgcct	tggattatag	taatttatgt	atatgtctat	1895
ttcatatact	ttaacctgaa	cccccttcaga	accatttctt	tttcatttct	taagttcttt	1955
gcacctagcc	cagtgccctgg	tacgtcgtgg	gtatttcagta	gattaaaaatg	cactttaagg	2015
aactttccctt	gttgtccatc	aagtggctaa	ggctctgtgc	tcccaatgca	ggggaccagg	2075
gttcaatctc	aggtcaggga	actagatccc	acaggtcaca	actaagagtt	tgcaagccac	2135
aactacctga	cctcacatgc	cacaactaat	cgaagatccc	tcgtgctgca	actaagtcct	2195
agtgacagtta	aatatatttt	tttaatgcac	tttgaatgtg	agaatgaatg	atgtgtcaca	2255
gacactgttg	tccccctgaga	agggagtgag	taatgatttg	agggccctca	tagtatatct	2315
tccttttttag ga ccc aga gac agg gac tgg ctt ggt gtc tca agg cag						2363
Gly Pro Arg Asp Arg Asp Trp Leu Gly Val Ser Arg Gln						
30 35						
ctc aga att aaa gca tgg aac aga cag ctg tat cca gag tgg aca gaa						2411
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu						
40 45 50						
agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc						2456
Ser Gln Gly Pro Asp Cys Trp Arg						
55 60						
agggaggata tgggtggaaat ggggtggggag ggggaacgggg ttgaatgtac ttaggaagat						2516
agggaaggaa aaggcataca gggaggagaa gccaaaggagc taattaatgc agctgccctt						2576
ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg						2625
Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu						
65 70 75						
att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc						2673
Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser						
80 85 90						
caa aag gtg ctg cca gat ggg cag gtc atc tgg gcc aac aac acc atc						2721
Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile						
95 100 105						
atc aat g gtgagtacct ctccgcctcc ttcccaagggt ccagaatccc tggtatcccc						2778
Ile Asn						
110						
aatgagctca aggaatcctc ctccctctttt tttttttttt tttttacaaa ttatatatgt						2838
aacacatatt cactgcagaa aaattagaaa acacagataa accaaaaaga aaaaaaatta						2898
tagttcccca aatggggcac agaagaccca gtggacatag aagttggata gacttggatt						2958
taaactgggt accagtatgt gaccctggac aagtcactga attgttttgt tcttccattc						3018
ccttatctat agaatgggga tgataacact ttaaaagggt cttgtaagga ttaaaatgtg						3078
ataatatata aagatttttag cataatgcct gccctgtgct gtgcttagta ccttagttta						3138
gacgctttgc aaccccatgg actgtagccc accaggctcc tctgtccatg tggattctgc						3198
aggcaagaat actggagtgg gtcaccatgc actcctccag gggatcttcc caactcaggg						3258
atcgaaccca ggtcctagcc tacagtatta attgatgctg ttattttttac ttttatccca						3318
ctagctagag cacatcatcc tagacatttt gatacatggc ctaccaattt gtgtccagtg						3378
taagaatata catgtgtgtg ctcaagtggct cagtcgtgtc tgactctttg caaccccatg						3438
gactgtagcc cgcgaaagct cctctgcccc tgggattgcc cagccaagaa tactggagca						3498
ggttgccatt tcttctcca ggggatcttt caacacaggg attgaatcct tgtctcctgt						3558
gtttcctgca ttggcagggt tattctttac cactgagcca cctgggaaac cccttaagta						3618
tatacacata aatctttttt agtttccatt ctcccctcta ccactccaaa taggttatac						3678
caaggagaat gtatttttgg agctaggcag tattctctga gccctctctt gggagtcatg						3738
ttaaagggttt tgggtgtacag tgaggaatgc cagggtattga gggagacttg ctgtcttctt						3798
ttcag gg agc cag gtg tgg gga gga cag ctg gta tat ccc caa gaa cct						3847
Gly Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro						
115 120 125						

SEQCRF05081156

gat gat acc tgc atc ttc ccc gat ggg gag ccc tgc cct tct ggc cct	3895
Asp Asp Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro	
130 135 140	
cta tct cag aaa aga tgc ttt gtt tat gtc tgg aag acc tgg g	3938
Leu Ser Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp	
145 150 155	
gtaagagttt cctttctctg gcctgtcatt cacacttaaa ttcacttctt cctacctgat	3998
ccccttttctt ttggtctcat ccttaaattc tgtgagtttc cctaattctt acttccccca	4058
tgactccttc ctcttccaca gcacctagtc aactctatta tacttctttc tgggagccct	4118
gctccaatta tagtcccatc ccattggacc tctcataagg acttttttcc tgcccaacat	4178
atgcaagctt aaactctctg aaataaccat ccttgataca tctcctgacc ttccttctct	4238
ggttccatct ctaaccctgc cccagtctcc tttgaccagt aacccccctt cctactcttc	4298
tttccaaaaa cctcag ac caa tac tgg caa gtt ctg ggg ggc cca gtg tct	4349
Asp Gln Tyr Trp Gln Val Leu Gly Gly Pro Val Ser	
160 165	
gga ctg agc atc ggg aca gac aag gca atg ctg ggc aca tat aac atg	4397
Gly Leu Ser Ile Gly Thr Asp Lys Ala Met Leu Gly Thr Tyr Asn Met	
170 175 180	
gaa gtg act gtc tac cac cgc cgg ggg tcc cag agc tat gtg ccc ctc	4445
Glu Val Thr Val Tyr His Arg Arg Gly Ser Gln Ser Tyr Val Pro Leu	
185 190 195 200	
gct cac tcc agt tca gcc ttc acc att act g gtaaggactg aggaggggac	4496
Ala His Ser Ser Ser Ala Phe Thr Ile Thr	
205 210	
aaggccagtt gcagggcagg agaaggtggg gaggctgggc tggacaggaa aggggaaaga	4556
ggaaatggtg tgtaacctta caggggcaga accaggaaga tgtgggcaga gggatgtggg	4616
gcttgagacc cgtgaagggc caggcagctt gggttggttg aaaaatatgg ctgtgaaaga	4676
agaagctgac agaaagaaga acttatgggt ctcactttct ctgactccaa tcccag ac	4734
Asp	
cag gtg ccc ttc tct gtg agt gtg tct cag ctg cag gcc ttg gat gga	4782
Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala Leu Asp Gly	
215 220 225	
agg aac aag cgc ttc ctg aga aag cag cct ctg acc ttt gcc ctc cag	4830
Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe Ala Leu Gln	
230 235 240	
ctc cat gat ccc agt ggc tat ttg gct ggg gct gac ctt tcc tac acc	4878
Leu His Asp Pro Ser Gly Tyr Leu Ala Gly Ala Asp Leu Ser Tyr Thr	
245 250 255	
tgg gac ttt ggt gac agt aca ggg acc ctg atc tct cgg gca ctc acg	4926
Trp Asp Phe Gly Asp Ser Thr Gly Thr Leu Ile Ser Arg Ala Leu Thr	
260 265 270 275	
gtc act cac act tac cta gag tct ggc cca gtc act gca cag gtg gtg	4974
Val Thr His Thr Tyr Leu Glu Ser Gly Pro Val Thr Ala Gln Val Val	
280 285 290	
ctg cag gct gcc att cct ctc acc tcc tgt ggc tcc tct cca gtt cca	5022
Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser Pro Val Pro	

SEQCRF05081156

295	300	305	
ggc act aca gat agg cat gtg aca act gca gag gct cct gga acc aca	5070		
Gly Thr Thr 310 Asp Arg His Val Thr 315 Thr Ala Glu Ala Pro 320 Gly Thr Thr			
gct ggc caa gtg cct act aca gaa gtc atg ggc acc aca cct ggc cag	5118		
Ala Gly Gln Val Pro Thr Thr 330 Glu Val Met Gly Thr 335 Thr Pro Gly Gln			
gtg cca act gca gag gcc cct ggc acc aca gtt ggg tgg gtg cca acc	5166		
Val Pro Thr Ala Glu Ala Pro Gly Thr Thr Val Gly Trp Val Pro Thr 355			
aca gag gat gta ggt acc aca cct gag cag gtg gca acc tcc aaa gtc	5214		
Thr Glu Asp Val Gly Thr Thr Pro Glu Gln Val Ala Thr Ser Lys Val 370			
tta agt aca aca cca gtg gag atg cca act gca aaa gct aca ggt agg	5262		
Leu Ser Thr Thr 375 Pro Val Glu Met Pro Thr Ala Lys Ala Thr 385 Gly Arg			
aca cct gaa gtg tca act aca gag ccc tct gga acc aca gtt aca cag	5310		
Thr Pro Glu Val Ser Thr Thr Glu Pro Ser Gly Thr Thr Val Thr Gln 400			
gga aca act cca gag ctg gtg gag acc aca gct gga gag gtg tcc act	5358		
Gly Thr Thr 405 Pro Glu Leu Val Glu Thr Thr Ala Gly Glu Val Ser Thr 415			
cct gag cct gcg ggt tca aat act agc tca ttc atg cct aca gaa ggt	5406		
Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser Phe 430 Met Pro Thr Glu Gly 435			
act gca g gtaagggggc caccatgaat gagttcatag aggtgggggca tttgtcacag	5463		
Thr Ala			
ctctgaagac ctgaaagaat tgctcaggac ccagatgtta ctcaatcctt agcttagcag	5523		
tgaggtcccc tcagaatctt cactgggtttt aaaaccccct aagtccctct taatggcaca	5583		
gaatagatcc agagttcagg aaaccagggt cttctcctag gccaggggta gagagcttat	5643		
tctctcttcc tgaagagaag ttcaggaagc agtgtgtgat catttggtgg tgggtgctcag	5703		
tcatgtctga ctctttgtga cctcatggac tatggcccac caggctcctc tgtccataga	5763		
attctccagg caagaacact ggagtggttg gccatttcct tctccagggg attttccctg	5823		
cccagggatt aaacccgaat tggcaggttg attctttacc cgagccacct agaaagtccc	5883		
atgtgatcat tagataatac ttataacctca ttttctgatt aagtgtaaac acagaaatct	5943		
ttctgacacc acttcccacc cctggatttc catcccaaag taggtttacc tgggaattgtg	6003		
gtaggaatac taaaaaggga gaagtgaat agtgacacta tgacttaaca catgtcaa	6063		
gtctgaccca ggacctggca cagtgtaggg tgtgataaac atttgggatg tctaaaattc	6123		
tgactctaac cctgtgactc tggggcagtc atttctcttg ggcctttctt tatcttaaaa	6183		
aatgagagtt tccagctctt gtctgattct aagcctggat ccagtagctc tgactctacc	6243		
tggaaaaatg cttgttgggc ctgttttcag gttagtcatt tgctttttga ctttgccctc	6303		
ttaatcctct cctccag gc tcc ctg agt ccc ctg ccg gat gac act gcc	6352		
Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala 440 445			
acc tta gtc ctg gag aag cgc caa gcc ccc ctg gat tgt gtt ctg tat	6400		
Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr 450 455 460			
cgc tat ggc tcc ttt tcc ctc acc ctg gac att gtc c gtgagtcttg	6447		
Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val 465 470 475			

## SEQCRF05081156

cctacattgt	ccgtaagctg	gtggagggag	gcgtgtgctg	cttaggggtg	cccagtggaa	6507
gcacaccttg	gaaggaatta	ctcacctgga	caaggagaat	acccagatcc	caggggtttc	6567
atatgaaggc	agaatgggat	tagggaggca	gcccgaggac	cttcctggcc	atgggccttg	6627
ggggaggata	agtagaggag	tctcagactt	aaaaaaatct	tgcaactttg	cag ag Gln	6682
ggt att gag agt gct gag atc cta cag gct gtg tca tcc agt gaa gga	6730					
Gly Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly						
480			485		490	
gat gca ttt gag ctg act gtg tct tgc caa ggc gg gtgagtgtcc	6775					
Asp Ala Phe Glu Leu Thr Val Ser Cys Gln Gly Gly						
495			500		505	
cacggttgcc	ctgagaactc	ctgggggtgac	tgctgtcctg	ttctctggtg	tctagtgtcc	6835
cttcccagat	tccctgacgt	aagctgacat	ctctcccag g	cta ccc aag gaa gcc	6890	
				Leu Pro Lys Glu Ala	510	
tgc atg gac atc tca tcg cca ggg tgt cag ctg cct gcc cag cgg ctg	6938					
Cys Met Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu						
515			520		525	
tgt cag cct gtg ccc ccc agc cca gcc tgc cag ctg gtt ttg cac cag	6986					
Cys Gln Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln						
530			535		540	
gta ctg aag ggt ggc tca ggg acc tac tgc ctc aat gtg tct ttg gct	7034					
Val Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala						
545			550		555	
gat gcc aat agc ctg gcg atg gtc agc acc cag ctt gtc atg cct g	7080					
Asp Ala Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro						
560			565		570	
gtaggtagtt	ggacaagagg	taggatgaag	acacggggag	atggtagagg	ttacctacta	7140
gaggaagcag	acactgaatg	cagccgtatc	tgggattcca	cccatag gg caa gaa	7195	
				Gly Gln Glu	575	
gca ggc ctc agg cag gct cct ctg ttc gtg ggc atc ttg ctg gtg cta	7243					
Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu Val Leu						
580			585		590	
aca gct ttg ttg ctt gca tct ctg ata tac ag gtgagatccc cgccatcctg	7295					
Thr Ala Leu Leu Ala Ser Leu Ile Tyr Arg						
595			600			
ctcccactcc	tttaccctt	attaccacca	ccactcttcc	tcattgggaag	aagaaaccac	7355
caaccctttt	gggaaagtgt	agagtccaag	aaagagccca	gacttggaag	ttcaacaggt	7415
ctaggctgca	gtcttgctgg	tgggaccctg	gggaagtcca	ttaacccttc	tgagccactg	7475
aaaagtagga	aacataatac	ctgtcctgtg	gggctgtttt	cagggctcta	gacaatgtga	7535
gtaaaacacc	tggttctgaa	acaaaagtgg	aataaatgat	gatctcaatg	actgttggtta	7595
tgaataatat	caacagtgga	gaagaactca	gtgaactgag	ttctccacct	gccagaaagg	7655
caaatcccta	ggcctggagg	gctgaggtcc	tcaaagcagg	gaagcctgta	gggtgagagg	7715
gaaatggtca	gagcttacca	taaacataag	agaggataaa	ccctgttggt	gagaagagga	7775
gggagccagg	atcaagacca	agtcaacctg	ggttatggtt	tagtcttttt	tttttagaga	7835
agcacaaaaga	ggttgccatt	gaccaccact	aaccagtatc	cctgcttttc	tcccaatatc	7895
ag g cga aga ctt atg aag caa ggc tca gca gtc ccc ctt ccc cag ctg	7943					

SEQCRF05081156

Arg Arg Leu Met Lys Gln Gly Ser Ala Val Pro Leu Pro Gln Leu  
605 610 615

cca cac ggt aga acc cag tgg cta cgt ctg ccc tgg gtc ttc cgc tct 7991  
Pro His Gly Arg Thr Gln Trp Leu Arg Leu Pro Trp Val Phe Arg Ser  
620 625 630

tgc ccc att ggt gag agc aaa ccc ctc ctc agt gga cag cag gtc 8036  
Cys Pro Ile Gly Glu Ser Lys Pro Leu Leu Ser Gly Gln Gln Val  
635 640 645

tgagtgtctt tatgtgaagt catgattttac ccaggtggac agcaaggcct gtctttttctc 8096  
tggtctttccc tcagagacta ccattgcctg aaataaagac tcagaacttg 8146

<210> 2  
<211> 649  
<212> PRT  
<213> Bos taurus

<400> 2  
Met Asp Leu Val Leu Arg Lys Tyr Leu Leu His Val Ala Leu Met Gly  
1 5 10 15  
Val Leu Leu Ala Val Gly Thr Thr Glu Gly Pro Arg Asp Arg Asp Trp  
20 25 30  
Leu Gly Val Ser Arg Gln Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu  
35 40 45  
Tyr Pro Glu Trp Thr Glu Ser Gln Gly Pro Asp Cys Trp Arg Gly Gly  
50 55 60  
His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala  
65 70 75 80  
Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser Gln Lys Val  
85 90 95  
Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile Ile Asn Gly  
100 105 110  
Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro Asp Asp  
115 120 125  
Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro Leu Ser  
130 135 140  
Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp Asp Gln Tyr Trp  
145 150 155 160  
Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Asp Lys  
165 170 175  
Ala Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr His Arg Arg  
180 185 190  
Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr  
195 200 205  
Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala  
210 215 220  
Leu Asp Gly Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe  
Page 7

SEQCRF05081156

225					230					235					240
Ala	Leu	Gln	Leu	His	Asp	Pro	Ser	Gly	Tyr	Leu	Ala	Gly	Ala	Asp	Leu
				245					250					255	
Ser	Tyr	Thr	Trp	Asp	Phe	Gly	Asp	Ser	Thr	Gly	Thr	Leu	Ile	Ser	Arg
			260					265					270		
Ala	Leu	Thr	Val	Thr	His	Thr	Tyr	Leu	Glu	Ser	Gly	Pro	Val	Thr	Ala
		275					280					285			
Gln	Val	Val	Leu	Gln	Ala	Ala	Ile	Pro	Leu	Thr	Ser	Cys	Gly	Ser	Ser
	290					295					300				
Pro	Val	Pro	Gly	Thr	Thr	Asp	Arg	His	Val	Thr	Thr	Ala	Glu	Ala	Pro
305					310					315					320
Gly	Thr	Thr	Ala	Gly	Gln	Val	Pro	Thr	Thr	Glu	Val	Met	Gly	Thr	Thr
				325					330					335	
Pro	Gly	Gln	Val	Pro	Thr	Ala	Glu	Ala	Pro	Gly	Thr	Thr	Val	Gly	Trp
			340					345					350		
Val	Pro	Thr	Thr	Glu	Asp	Val	Gly	Thr	Thr	Pro	Glu	Gln	Val	Ala	Thr
		355					360					365			
Ser	Lys	Val	Leu	Ser	Thr	Thr	Pro	Val	Glu	Met	Pro	Thr	Ala	Lys	Ala
	370					375					380				
Thr	Gly	Arg	Thr	Pro	Glu	Val	Ser	Thr	Thr	Glu	Pro	Ser	Gly	Thr	Thr
385					390					395					400
Val	Thr	Gln	Gly	Thr	Thr	Pro	Glu	Leu	Val	Glu	Thr	Thr	Ala	Gly	Glu
				405					410					415	
Val	Ser	Thr	Pro	Glu	Pro	Ala	Gly	Ser	Asn	Thr	Ser	Ser	Phe	Met	Pro
			420					425					430		
Thr	Glu	Gly	Thr	Ala	Gly	Ser	Leu	Ser	Pro	Leu	Pro	Asp	Asp	Thr	Ala
		435					440					445			
Thr	Leu	Val	Leu	Glu	Lys	Arg	Gln	Ala	Pro	Leu	Asp	Cys	Val	Leu	Tyr
	450					455					460				
Arg	Tyr	Gly	Ser	Phe	Ser	Leu	Thr	Leu	Asp	Ile	Val	Gln	Gly	Ile	Glu
465					470					475					480
Ser	Ala	Glu	Ile	Leu	Gln	Ala	Val	Ser	Ser	Ser	Glu	Gly	Asp	Ala	Phe
				485					490					495	
Glu	Leu	Thr	Val	Ser	Cys	Gln	Gly	Gly	Leu	Pro	Lys	Glu	Ala	Cys	Met
			500					505					510		
Asp	Ile	Ser	Ser	Pro	Gly	Cys	Gln	Leu	Pro	Ala	Gln	Arg	Leu	Cys	Gln
		515					520					525			
Pro	Val	Pro	Pro	Ser	Pro	Ala	Cys	Gln	Leu	Val	Leu	His	Gln	Val	Leu
	530					535					540				
Lys	Gly	Gly	Ser	Gly	Thr	Tyr	Cys	Leu	Asn	Val	Ser	Leu	Ala	Asp	Ala
545					550					555					560



SEQCRF05081156

Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro Gly Gln Glu  
565 570 575  
Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu Val Leu  
580 585 590  
Thr Ala Leu Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys  
595 600 605  
Gln Gly Ser Ala Val Pro Leu Pro Gln Leu Pro His Gly Arg Thr Gln  
610 615 620  
Trp Leu Arg Leu Pro Trp Val Phe Arg Ser Cys Pro Ile Gly Glu Ser  
625 630 635 640  
Lys Pro Leu Leu Ser Gly Gln Gln Val  
645

<210> 3  
<211> 8146  
<212> DNA  
<213> Bos taurus

<220>  
<221> CDS  
<222> (30)..(104)  
<223> First CDS region

<220>  
<221> CDS  
<222> (2326)..(2435)  
<223> Second CDS region

<220>  
<221> CDS  
<222> (2582)..(2727)  
<223> Third CDS region

<220>  
<221> CDS  
<222> (3804)..(3937)  
<223> Fourth CDS region

<220>  
<221> CDS  
<222> (4314)..(4475)  
<223> Fifth CDS region

<220>  
<221> CDS  
<222> (4732)..(5412)  
<223> Sixth CDS region

<220>  
<221> CDS  
<222> (6321)..(6436)  
<223> Seventh CDS region

<220>  
<221> CDS  
<222> (6681)..(6765)  
<223> Eighth CDS region

## SEQCRF05081156

<220>  
 <221> CDS  
 <222> (6876)..(7079)  
 <223> Ninth CDS region

<220>  
 <221> CDS  
 <222> (7188)..(7275)  
 <223> Tenth CDS region

<220>  
 <221> CDS  
 <222> (7899)..(8036)  
 <223> Eleventh CDS region

<400> 3  
 ggtcttttggg tgctggaagg aagaacagg atg gat ctg gtg ctg aga aaa tac 53  
 Met Asp Leu Val Leu Arg Lys Tyr  
 1 5

ctt ctc cat gtg gct ctg atg ggt gtt ctt ctg gct gta agg acc aca 101  
 Leu Leu His Val Ala Leu Met Gly Val Leu Leu Ala Val Arg Thr Thr  
 10 15 20

gaa g gtgagtgtgg gatgttggac atgaacaagt gtgaatttgg gggtgcacac 155  
 Glu  
 25

ctgctctggt	ttttctctcc	ctaaaatgga	agatatcagt	agtgccttcag	gtgtctccca	215
cccatttgat	ttagtgagga	catgggcaac	tgagctccct	ccccacatga	agatttgggt	275
gcatgtgtgt	tcaggcacct	gggactgaac	ctgaaaacaa	ccccatctac	ctggatgggt	335
gagagaacag	tatgtctccg	tggccctaata	tttgagatgc	tctgaatagt	gagctggaac	395
atgggtgccca	aggtagtaaa	atgagtggaa	actcatttag	gctttgtctc	aggcacttgg	455
gatagggtat	ttaggagata	gagaaagata	ggagatagga	gaaaggagaa	agaggatgtg	515
gtattggata	gaagggtaat	gaggcacctc	atccccctct	tgggatgggc	atgggtgaac	575
acagcccagg	cttttgttct	ggggctggaa	gagacaggca	gaaggggtctc	agctgagcat	635
cacatgaaag	ggctctgggg	gattggggcc	tcgtgacagg	agcaaggcgg	gtgggggtggg	695
gatggtgaga	gggtctggaa	tgtcccgtgc	tgctctgagg	agggaggatt	gggagtggag	755
aaagaatggg	gcatcttatg	attctcttgt	tcttgtgtgt	aggtattcag	tgggataatt	815
ctagatcctc	ccccaaagaga	atcaaccagg	tttctggtac	atgttagaga	tggagtgagg	875
atagtctgtg	atgtgcagaa	atatctacat	tgtaccccag	tgcccccttt	ctctagatcc	935
ctggtctcac	agacttcttg	gaacttctcc	ttgatctgac	ttccctcatt	catggtgtca	995
ttttcaagctt	tattctttta	ctatgttcgt	tattgtattc	tggaaatata	ctgttcatat	1055
gtgtccaccc	aaggctctta	atatgttgtg	cttacttttt	ggatccagat	ttttaaaatc	1115
ataagaagac	atttttatat	agttcatgaa	attttgcatt	gactgagttt	gataattttg	1175
tttagtgtga	attaacattg	tgtttattta	agaaaaaaaa	atattttttt	acagaaacct	1235
actgaatttg	taggggtttta	aaataacatg	atgtctggga	tttgcttttg	aatgcttcag	1295
ccaaaaaaca	aacgaacaac	aaaaataaag	gatagataaa	gcaaattgtga	caaaatgctg	1355
atagttgttg	gaccttgagg	agacacatgc	agagccatca	catcactttt	tttcagacat	1415
ctttcttggg	cagttataat	cattttgttt	gtccccactc	ccaatttcta	cttgccctcta	1475
gtccatcctc	ctcactgctt	gccaaagtga	tccttctaaa	acacaaatct	gatcatattc	1535
aaaaagcttt	tgaagggtaa	gttttatggg	atatgccata	tatcagtaca	acaaacaaaa	1595
tcgtctgagg	tgccgttgcc	tacaggataa	agtccaaact	cctttgcctg	gcactccaag	1655
cccccatctt	atcttcttgg	cctcatctct	catgatgtac	atcagccaca	ttgctagtgt	1715
ctgctcatgg	ccttctgcct	agaatgcttt	atgccccagc	caactattta	ctgtcttctt	1775
cagtcgacca	gagtgcgaatt	tacctgttta	aaatctatca	ttttgttata	cattgtgcat	1835
gtctattatg	gctcatatta	agcaatgcct	tggattatag	taattttatg	atatgtctat	1895
ttcatatact	ttaacctgaa	ccccttcaga	accatttctt	tttcatttct	taagttcttt	1955
gcacctagcc	cagtgccctg	tacgtcgtgg	gtatttcagta	gattaaaaatg	cactttaagg	2015
aactttccctt	gttgtccatc	aagtggctaa	ggctctgtgc	tcccaatgca	ggggaccagg	2075
gttcaacttc	aggtcaggga	actagatccc	acaggtcaca	actaagagtt	tgcaagccac	2135
aactacctga	cctcacatgc	cacaactaat	cgaagatccc	tcgtgctgca	actaagtcct	2195

SEQCRF05081156

agtgacagttta aatatatattt ttttaatgcac tttgaatgtg agaataaatg atgtgtgcaca	2255
gacactgttg tcccctgaga agggagtgag taatgatttg agggccctca tagtatatct	2315
tccttttttag ga ccc aga gac agg gac tgg ctt ggt gtc tca agg cag	2363
Gly Pro Arg Asp Arg Asp Trp Leu Gly Val Ser Arg Gln	
30 35	
ctc aga att aaa gca tgg aac aga cag ctg tat cca gag tgg aca gaa	2411
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu	
40 45 50	
agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc	2456
Ser Gln Gly Pro Asp Cys Trp Arg	
55 60	
agggaggata tgggtggaaat ggggtggggag ggggaacgggg ttgaatgtac ttaggaagat	2516
aggggaaggaa aaggcataca gggaggagaa gccaaaggagc taattaatgc agctgccctt	2576
ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg	2625
Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu	
65 70 75	
att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc	2673
Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser	
80 85 90	
caa aag gtg ctg cca gat ggg cag gtc atc tgg gcc aac aac acc atc	2721
Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile	
95 100 105	
atc aat g gtgagtacct ctccgcctcc ttcccaagggt ccagaatccc tggtatcccc	2778
Ile Asn	
110	
aatgagctca aggaatcctc ctctcttttt tttttttttt tttttacaaa ttatatatgt	2838
aacacatatatt cactgcagaa aaattagaaa acacagataa accaaaaaga aaaaaaatta	2898
tagttcccca aatggggcac agaagaccca gtggacatag aagtttgata gacttggaatt	2958
taaactgggtt accagtatgt gaccctggac aagtcactga attgttttgt tcttccattc	3018
ccttatctat agaatgggga tgataacact ttaaaagggtt cttgtaagga ttaaaatgtg	3078
ataatatata aagatttttag cataatgcct gccctgtgct gtgcttagta ccttagttta	3138
gacgctttgc aaccccatgg actgtagccc accaggctcc tctgtccatg tggattctgc	3198
aggcaagaat actggagtggt gtcaccatgc actcctccag gggatcttcc caactcaggg	3258
atcgaaccca ggtcctagcc tacagtatta attgatgctg ttattttttac ttttatccca	3318
ctagctagag cacatcatcc tagacatttt gatacatggc ctaccaattht gtgtccagt	3378
taagaatata catgtgtgtg ctcatgtggt cagtcgtgtc tgactctttg caaccccatg	3438
gactgtagcc cgcgaaagct cctctgcccc tgggattgcc cagccaagaa tactggagca	3498
ggttgccatt tcttcttcca ggggatcttt caacacagggt attgaatcct tgtctcctgt	3558
gtttcctgca ttggcagggtg tattctttac cactgagcca cctgggaaac cccttaagta	3618
tatacacata aatctttttat agtttccatt ctcccttcta ccaactccaaa taggttatac	3678
caaggagaat gtatttttgt agctaggcag tatttcttga gcccctctct gggagtcattg	3738
ttaaaggttt tgggtgtacag tgaggaatgc cagggattga gggagacttg ctgtcttctt	3798
ttcag gg agc cag gtg tgg gga gga cag ctg gta tat ccc caa gaa cct	3847
Gly Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro	
115 120 125	
gat gat acc tgc atc ttc ccc gat ggg gag ccc tgc cct tct ggc cct	3895
Asp Asp Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro	
130 135 140	
cta tct cag aaa aga tgc ttt gtt tat gtc tgg aag acc tgg g	3938
Leu Ser Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp	
145 150 155	

SEQCRF05081156

gtaagagttt	cccttctctg	gcctgtcatt	cacacttaaa	ttcacttctt	cctacctgat	3998										
cccccttctt	ttggtctcat	ccttaaattc	tgtgagtttc	cctaattctt	acttccccca	4058										
tgactccttc	ctcttccaca	gcacctagtc	aactctatta	tacttctttc	tgggagccct	4118										
gctccaatta	tagtcccatc	ccatggaccc	tctcataagg	acttttttcc	tgcccaacat	4178										
atgcaagctt	aaactctctg	aaataaccat	ccttgataca	tctcctgacc	ttccttctct	4238										
ggttccatct	ctaaccctgc	cccagtctcc	tttgaccagt	aacccccctt	cctactcttc	4298										
tttccaaaaa	cctcag	ac	caa	tac	tgg	caa	gtt	ctg	ggg	ggc	cca	gtg	tct	4349		
	Asp	Gln	Tyr	Trp	Gln	Val	Leu	Gly	Gly	Pro	Val	Ser				
					160								165			
gga	ctg	agc	atc	ggg	aca	gac	aag	gca	atg	ctg	ggc	aca	tat	aac	atg	4397
Gly	Leu	Ser	Ile	Gly	Thr	Asp	Lys	Ala	Met	Leu	Gly	Thr	Tyr	Asn	Met	
	170					175					180					
gaa	gtg	act	gtc	tac	cac	cgc	cgg	ggg	tcc	cag	agc	tat	gtg	ccc	ctc	4445
Glu	Val	Thr	Val	Tyr	His	Arg	Arg	Gly	Ser	Gln	Ser	Tyr	Val	Pro	Leu	
	185				190					195					200	
gct	cac	tcc	agt	tca	gcc	ttc	acc	att	act	g	gtaaggactg	aggaggggac				4496
Ala	His	Ser	Ser	Ser	Ala	Phe	Thr	Ile	Thr							
				205					210							
aaggccagtt	gcagggcagg	agaaggtggg	gaggctgggc	tggacaggaa	aggggaaaga	4556										
ggaaatggtg	tgtaacctta	caggggcaga	accaggaaga	tgtgggcaga	gggatgtggg	4616										
gcttgagacc	cgtgaagggc	caggcagctt	gggttggttg	aaaaatatgg	ctgtgaaaga	4676										
agaagctgac	agaaagaaga	acttatgggtt	ctcacttttct	ctgactccaa	tccca	gac										4734
						Asp										
cag	gtg	ccc	ttc	tct	gtg	agt	gtg	tct	cag	ctg	cag	gcc	ttg	gat	gga	4782
Gln	Val	Pro	Phe	Ser	Val	Ser	Val	Ser	Gln	Leu	Gln	Ala	Leu	Asp	Gly	
			215					220					225			
agg	aac	aag	cgc	ttc	ctg	aga	aag	cag	cct	ctg	acc	ttt	gcc	ctc	cag	4830
Arg	Asn	Lys	Arg	Phe	Leu	Arg	Lys	Gln	Pro	Leu	Thr	Phe	Ala	Leu	Gln	
		230					235					240				
ctc	cat	gat	ccc	agt	ggc	tat	ttg	gct	ggg	gct	gac	ctt	tcc	tac	acc	4878
Leu	His	Asp	Pro	Ser	Gly	Tyr	Leu	Ala	Gly	Ala	Asp	Leu	Ser	Tyr	Thr	
	245					250					255					
tgg	gac	ttt	ggt	gac	agt	aca	ggg	acc	ctg	atc	tct	cgg	gca	ctc	acg	4926
Trp	Asp	Phe	Gly	Asp	Ser	Thr	Gly	Thr	Leu	Ile	Ser	Arg	Ala	Leu	Thr	
	260				265					270					275	
gtc	act	cac	act	tac	cta	gag	tct	ggc	cca	gtc	act	gca	cag	gtg	gtg	4974
Val	Thr	His	Thr	Tyr	Leu	Glu	Ser	Gly	Pro	Val	Thr	Ala	Gln	Val	Val	
				280					285					290		
ctg	cag	gct	gcc	att	cct	ctc	acc	tcc	tgt	ggc	tcc	tct	cca	gtt	cca	5022
Leu	Gln	Ala	Ala	Ile	Pro	Leu	Thr	Ser	Cys	Gly	Ser	Ser	Pro	Val	Pro	
			295					300					305			
ggc	act	aca	gat	agg	cat	gtg	aca	act	gca	gag	gct	cct	gga	acc	aca	5070
Gly	Thr	Thr	Asp	Arg	His	Val	Thr	Thr	Ala	Glu	Ala	Pro	Gly	Thr	Thr	
		310					315					320				
gct	ggc	caa	gtg	cct	act	aca	gaa	gtc	atg	ggc	acc	aca	cct	ggc	cag	5118
Ala	Gly	Gln	Val	Pro	Thr	Thr	Glu	Val	Met	Gly	Thr	Thr	Pro	Gly	Gln	
	325					330					335					

SEQCRF05081156

gtg cca act gca gag gcc cct ggc acc aca gtt ggg tgg gtg cca acc Val Pro Thr Ala Glu Ala Pro Gly Thr Thr Val Gly Trp Val Pro Thr 340 345 350 355	5166
aca gag gat gta ggt acc aca cct gag cag gtg gca acc tcc aaa gtc Thr Glu Asp Val Gly Thr Thr Pro Glu Gln Val Ala Thr Ser Lys Val 360 365 370	5214
tta agt aca aca cca gtg gag atg cca act gca aaa gct aca ggt agg Leu Ser Thr Thr Pro Val Glu Met Pro Thr Ala Lys Ala Thr Gly Arg 375 380 385	5262
aca cct gaa gtg tca act aca gag ccc tct gga acc aca gtt aca cag Thr Pro Glu Val Ser Thr Thr Glu Pro Ser Gly Thr Thr Val Thr Gln 390 395 400	5310
gga aca act cca gag ctg gtg gag acc aca gct gga gag gtg tcc act Gly Thr Thr Pro Glu Leu Val Glu Thr Thr Ala Gly Glu Val Ser Thr 405 410 415	5358
cct gag cct gcg ggt tca aat act agc tca ttc atg cct aca gaa ggt Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser Phe Met Pro Thr Glu Gly 420 425 430 435	5406
act gca g gtaagggggc caccatgaat gagttcatag aggtggggca tttgtcacag Thr Ala	5463
ctctgaagac ctgaaagaat tgctcaggac ccagatgtta ctcaatcctt agcttagcag tggagtcccc tcagaatctt cactggtttt aaaaccccct aagtccctct taatggcaca gaatagatcc agagttcagg aaaccagggt cttctcctag gccaggggta gagagcttat tctctcttcc tgaagagaag ttcaggaagc agtgtgtgat catttggtgg tgggtgctcag tcatgtctga ctctttgtga cctcatggac tatggcccac caggctcctc tgtccataga attctccagg caagaacact ggagtgggtg gccatttcct tctccagggg attttccctg cccagggatt aaaccggaat tggcagggtg attctttacc cgagccacct agaaagtccc atgtgatcat tagataatac ttatacctca ttttctgatt aagtgtaaac acagaaatct ttctgacacc acttcccacc cctggattcc catcccaaag taggtttacc tgggaattgtg gtaggaatac taaaaaggga gaagtgaat agtgacacta tgacttaaca catgtcaaat gtctgaccca ggacctggca cagtgtaggg tgtgataaac atttgggatg tctaaaattc tgactctaac cctgtgactc tggggcagtc atttctcttg ggcctttctt tatcttaaaa aatgagagtt tccagctctt gtctgattct aagcctggat ccagtagctc tgactctacc tggaaaaaatg cttgttgggc ctgttttcag gttagtcatt tgctttttga ctttgcctct	5523 5583 5643 5703 5763 5823 5883 5943 6003 6063 6123 6183 6243 6303
ttaatcctct cctccag gc tcc ctg agt ccc ctg ccg gat gac act gcc Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala 440 445	6352
acc tta gtc ctg gag aag cgc caa gcc ccc ctg gat tgt gtt ctg tat Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr 450 455 460	6400
cgc tat ggc tcc ttt tcc ctc acc ctg gac att gtc c gtgagtcttg Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val 465 470 475	6447
cctacattgt ccgtaagctg gtggagggag gcgtgtgctg cttaggggtg cccagtggaa gcacaccttg gaaggaatta ctcacctgga caaggagaat acccagatcc caggggtttc atatgaaggc agaattgggat tagggaggca gcccaggagac cttcctggcc atgggccttg	6507 6567 6627
ggggaggata agtagaggag tctcagactt aaaaaaatct tgcaactttg cag ag Gln	6682

SEQCRF05081156

ggt att gag agt gct gag atc cta cag gct gtg tca tcc agt gaa gga Gly Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly 480 485 490	6730
gat gca ttt gag ctg act gtg tct tgc caa ggc gg gtgagtgtcc Asp Ala Phe Glu Leu Thr Val Ser Cys Gln Gly Gly 495 500 505	6775
cacggttgcc ctgagaactc ctggggtgac tgctgtcctg ttctctggtg tctagtgtcc	6835
cttcccagat tccctgacgt aagctgacat ctctcccag g cta ccc aag gaa gcc Leu Pro Lys Glu Ala 510	6890
tgc atg gac atc tca tcg cca ggg tgt cag ctg cct gcc cag cgg ctg Cys Met Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu 515 520 525	6938
tgt cag cct gtg ccc ccc agc cca gcc tgc cag ctg gtt ttg cac cag Cys Gln Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln 530 535 540	6986
gta ctg aag ggt ggc tca ggg acc tac tgc ctc aat gtg tct ttg gct Val Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala 545 550 555	7034
gat gcc aat agc ctg gcg atg gtc agc acc cag ctt gtc atg cct g Asp Ala Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro 560 565 570	7080
gtaggtagtt ggacaagagg taggatgaag acacggggag atggtagagg ttacctacta	7140
gaggaagcag acactgaatg cagccgtatc tgggattcca cccatag gg caa gaa Gly Gln Glu 575	7195
gca ggc ctc agg cag gct cct ctg ttc gtg ggc atc ttg ctg gtg cta Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu Val Leu 580 585 590	7243
aca gct ttg ttg ctt gca tct ctg ata tac ag gtgagatccc cgccatcctg Thr Ala Leu Leu Leu Ala Ser Leu Ile Tyr Arg 595 600	7295
ctcccactcc tttacccttt attaccacca ccactcttcc tcatgggaag aagaaaccac caaccctttt gggaaagtgt agagtccaag aaagagccca gacttggaag ttcaacaggt ctaggctgca gtcttgcttg tgggaccctg ggggaagtcca ttaacccttc tgagccactg aaaagttaga aacataatac ctgtcctgtg gggctgtttt cagggtctta gacaatgtga gtaaaacacc tggttctgaa acaaaagtgg aataaatgat gatctcaatg actggttgta tgaataatat caacagtgga gaagaactca gtgaactgag ttctccacct gccagaaagg caaatcccta ggcctggagg gctgaggtcc tcaaagcagg gaagcctgta gggtagagagg gaaatggtca gagcttacca taaacataag agaggataaa ccctgttggt gagaagagga gggagccagg atcaagacca agtcaacctg gggttatggtt tagtcttttt tttttagaga agcacaaaaga ggttgccatt gaccaccact aaccagtatc cctgcttttc tcccaatatc	7355 7415 7475 7535 7595 7655 7715 7775 7835 7895
ag g cga aga ctt atg aag caa ggc tca gca gtc ccc ctt ccc cag ctg Arg Arg Leu Met Lys Gln Gly Ser Ala Val Pro Leu Pro Gln Leu 605 610 615	7943
cca cac ggt aga acc cag tgg cta cgt ctg ccc tgg gtc ttc cgc tct Pro His Gly Arg Thr Gln Trp Leu Arg Leu Pro Trp Val Phe Arg Ser	7991

SEQCRF05081156

620

625

630

tgc ccc att ggt gag agc aaa ccc ctc ctc agt gga cag cag gtc 8036  
Cys Pro Ile Gly Glu Ser Lys Pro Leu Leu Ser Gly Gln Gln Val  
635 640 645

tgagtgtctt tatgtgaagt catgattttac ccaggtggac agcaaggcct gtctttttctc 8096  
tggtctttccc tcagagacta ccattgcctg aaataaagac tcagaacttg 8146

<210> 4  
<211> 649  
<212> PRT  
<213> Bos taurus

<400> 4  
Met Asp Leu Val Leu Arg Lys Tyr Leu Leu His Val Ala Leu Met Gly  
1 5 10 15  
Val Leu Leu Ala Val Arg Thr Thr Glu Gly Pro Arg Asp Arg Asp Trp  
20 25 30  
Leu Gly Val Ser Arg Gln Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu  
35 40 45  
Tyr Pro Glu Trp Thr Glu Ser Gln Gly Pro Asp Cys Trp Arg Gly Gly  
50 55 60  
His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala  
65 70 75 80  
Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser Gln Lys Val  
85 90 95  
Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile Ile Asn Gly  
100 105 110  
Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro Asp Asp  
115 120 125  
Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro Leu Ser  
130 135 140  
Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp Asp Gln Tyr Trp  
145 150 155 160  
Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Asp Lys  
165 170 175  
Ala Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr His Arg Arg  
180 185 190  
Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr  
195 200 205  
Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala  
210 215 220  
Leu Asp Gly Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe  
225 230 235 240  
Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Gly Ala Asp Leu  
245 250 255

SEQCRF05081156

Ser	Tyr	Thr	Trp 260	Asp	Phe	Gly	Asp	Ser 265	Thr	Gly	Thr	Leu	Ile 270	Ser	Arg	
Ala	Leu	Thr 275	Val	Thr	His	Thr	Tyr 280	Leu	Glu	Ser	Gly	Pro 285	Val	Thr	Ala	
Gln	Val 290	Val	Leu	Gln	Ala	Ala 295	Ile	Pro	Leu	Thr	Ser 300	Cys	Gly	Ser	Ser	
Pro 305	Val	Pro	Gly	Thr	Thr 310	Asp	Arg	His	Val	Thr 315	Thr	Ala	Glu	Ala	Pro 320	
Gly	Thr	Thr	Ala	Gly 325	Gln	Val	Pro	Thr	Thr 330	Glu	Val	Met	Gly	Thr 335	Thr	
Pro	Gly	Gln	Val 340	Pro	Thr	Ala	Glu	Ala 345	Pro	Gly	Thr	Thr	Val 350	Gly	Trp	
Val	Pro	Thr 355	Thr	Glu	Asp	Val	Gly 360	Thr	Thr	Pro	Glu	Gln 365	Val	Ala	Thr	
Ser	Lys 370	Val	Leu	Ser	Thr	Thr 375	Pro	Val	Glu	Met	Pro 380	Thr	Ala	Lys	Ala	
Thr 385	Gly	Arg	Thr	Pro	Glu 390	Val	Ser	Thr	Thr	Glu 395	Pro	Ser	Gly	Thr	Thr 400	
Val	Thr	Gln	Gly	Thr 405	Thr	Pro	Glu	Leu	Val 410	Glu	Thr	Thr	Ala	Gly 415	Glu	
Val	Ser	Thr	Pro 420	Glu	Pro	Ala	Gly	Ser 425	Asn	Thr	Ser	Ser	Phe 430	Met	Pro	
Thr	Glu	Gly 435	Thr	Ala	Gly	Ser	Leu 440	Ser	Pro	Leu	Pro	Asp 445	Asp	Thr	Ala	
Thr	Leu 450	Val	Leu	Glu	Lys	Arg 455	Gln	Ala	Pro	Leu	Asp 460	Cys	Val	Leu	Tyr	
Arg 465	Tyr	Gly	Ser	Phe	Ser 470	Leu	Thr	Leu	Asp	Ile 475	Val	Gln	Gly	Ile	Glu 480	
Ser	Ala	Glu	Ile 485	Leu	Gln	Ala	Val	Ser	Ser 490	Ser	Glu	Gly	Asp	Ala 495	Phe	
Glu	Leu	Thr	Val 500	Ser	Cys	Gln	Gly	Gly 505	Leu	Pro	Lys	Glu	Ala 510	Cys	Met	
Asp	Ile	Ser 515	Ser	Pro	Gly	Cys	Gln 520	Leu	Pro	Ala	Gln	Arg 525	Leu	Cys	Gln	
Pro	Val 530	Pro	Pro	Ser	Pro	Ala 535	Cys	Gln	Leu	Val	Leu 540	His	Gln	Val	Leu	
Lys 545	Gly	Gly	Ser	Gly	Thr 550	Tyr	Cys	Leu	Asn	Val 555	Ser	Leu	Ala	Asp	Ala 560	
Asn	Ser	Leu	Ala	Met 565	Val	Ser	Thr	Gln	Leu 570	Val	Met	Pro	Gly	Gln 575	Glu	
Ala	Gly	Leu	Arg 580	Gln	Ala	Pro	Leu	Phe 585	Val	Gly	Ile	Leu	Leu 590	Val	Leu	



SEQCRF05081156

Thr Ala Leu Leu Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys  
           595                          600                          605  
 Gln Gly Ser Ala Val Pro Leu Pro Gln Leu Pro His Gly Arg Thr Gln  
       610                          615                          620  
 Trp Leu Arg Leu Pro Trp Val Phe Arg Ser Cys Pro Ile Gly Glu Ser  
   625                          630                          635                          640  
 Lys Pro Leu Leu Ser Gly Gln Gln Val  
                           645

<210> 5  
 <211> 8143  
 <212> DNA  
 <213> Bos taurus

<220>  
 <221> CDS  
 <222> (30)..(101)  
 <223> First CDS region

<220>  
 <221> CDS  
 <222> (2323)..(2432)  
 <223> Second CDS region

<220>  
 <221> CDS  
 <222> (2579)..(2724)  
 <223> Third CDS region

<220>  
 <221> CDS  
 <222> (3801)..(3934)  
 <223> Fourth CDS region

<220>  
 <221> CDS  
 <222> (4312)..(4472)  
 <223> Fifth CDS region

<220>  
 <221> CDS  
 <222> (4730)..(5409)  
 <223> Sixth CDS region

<220>  
 <221> CDS  
 <222> (6318)..(6433)  
 <223> Seventh CDS region

<220>  
 <221> CDS  
 <222> (6678)..(6762)  
 <223> Eighth CDS region

<220>  
 <221> CDS  
 <222> (6873)..(7076)  
 <223> Ninth CDS region

SEQCRF05081156

```
<220>
<221> CDS
<222> (7185)..(7272)
<223> Tenth CDS region
```

```
<220>
<221> CDS
<222> (7896)..(8033)
<223> Eleventh CDS region
```

<400> 5  
ggctcttggg tgctggaagg aagaacagg atg gat ctg gtg ctg aga aaa tac 53  
Met Asp Leu Val Leu Arg Lys Tyr  
1 5

ctt ctc cat gtg gct ctg atg ggt gtt ctg gct gta ggg acc aca gaa g 102  
Leu Leu His Val Ala Leu Met Gly Val Leu Ala Val Gly Thr Thr Glu  
10 15 20

gtgagtgtgg	gatgttggac	atgaacaagt	gtgaatttgg	ggttgcacac	ctgctctggt	162
ttttctctcc	ctaaaatgga	agatatcagt	agtgtctcag	gtgtctccca	cccatttgat	222
ttagtgagga	catgggcaac	tgagctccct	ccccacatga	agatttgggt	gcatgtgtgt	282
tcaggcactt	gggactgaac	ctgaaaaaca	ccccatctac	ctggatgggt	gagagaacag	342
tatgtctccg	tggccctaatt	tttgatagtc	tctgaatagt	gagctggaac	atgggtgccca	402
aggtagtaaa	atgagtggaa	actcatttag	gctttgtctc	aggcatttgg	gatagggtat	462
ttaggagata	gagaaagata	ggagatagga	gaaaggagaa	agaggatgtg	gtattggata	522
gaagggtaat	gaggcacctc	atccccctct	tgggatgggc	atgggtgaac	acagcccagg	582
cttttgttct	ggggctggaa	gagacaggca	gaagggtctc	agctgagcat	cacatgaaag	642
ggctctgggg	gattggggcc	tcgtgacagg	agcaaggcgg	gtggggtggg	gatggtgaga	702
gggtctggaa	tgtcccgtgc	tgtctcaggg	agggaggatt	gggagtgagg	aaagaatggg	762
gcatctttatg	attctcttgt	tcttgtggtg	aggtattcag	tgggataatt	ctagatcctc	822
ccccaagaga	atcaaccagg	tttctggtac	atgttagaga	tggagtgagg	atagtctgtg	882
atgtgcagaa	atatctacat	tgtaccccag	tgcccccttt	ctctagatcc	ctggtctcac	942
agacttcttg	gaacttctcc	ttgatctgac	ttccctcatt	catggtgtca	tttcaagtct	1002
tattctttta	ctatgttcgt	tattgtattc	tggaaatatc	ctgttcatat	gtgtccaccc	1062
aaagctctta	atatgttgtg	cttacttttt	ggatccagat	ttttaaaatc	ataagaagac	1122
atttttatat	agttcatgaa	attttgcattg	gactgagttt	gataattttg	tttagtgtga	1182
attaacattg	tgtttattta	agaaaaaaaa	atattttttt	acagaaacct	actgaatttg	1242
tagggtttta	aaataacatg	atgtctggga	tttgcttttg	aatgcttcag	ccaaaaaaca	1302
aacgaacaac	aaaaataaag	gatagataaa	gcaaatgtga	caaaatgctg	atagttgttg	1362
gacctttggg	agacacatgc	agagccatca	catacttttt	tttcagacat	cttttcttgg	1422
cagttataat	cattttgttt	gtccccactc	ccaatttcta	cttgcttcta	gtccactctc	1482
ctcactgctt	gccaaagtga	tccttctaaa	acacaaatct	gatcatattc	aaaaagcttt	1542
tgaagggtaa	gttttatggt	atatgccata	tatcagtaca	acaaacaaaa	tcgtctgagg	1602
tgccgttgcc	tacaggataa	agtccaaact	cctttgcctg	gcactccaag	ccccactct	1662
atcttcttgg	cctcatctct	catgatgtac	atcagccaca	ttgctagtgt	ctgctcatgg	1722
ccttctgcct	agaatgcttt	atgccccagc	caactattta	ctgttcttct	cagtcgacca	1782
gagtgcaatt	tacctgttta	aaacttatca	ttttgttata	tatgtgtcat	gtctattatg	1842
gctcatatta	agcaatgcct	tggattatag	taatttatgt	atatgtctat	ttcatatact	1902
ttaacctgaa	ccccttcaga	accattttct	tttcatttct	taagttcttt	gcacctagcc	1962
cagtgcctgg	tacgtcgtgg	gtattcagta	gattaaaaatg	cactttaagg	aacttccctt	2022
gttggtccatc	aagtggctaa	ggctctgtgc	tcccaatgca	ggggaccagg	gttcaatctc	2082
aggtcaggga	actagatccc	acagggtcac	actaagagtt	tgcaagccac	aactacctga	2142
ccacacatgc	cacaactaat	cgaagatccc	tcgtgtcgca	actaagtcct	agtgacgtta	2202
aatatatttt	tttaatgcac	tttgaatgtg	agaatgaatg	atgtgtcaca	gacactgttg	2262
tcccctgaga	agggagtgg	taatgatttg	agggccctca	tagtatatct	tccttttttag	2322

ga ccc aga gac agg gac tgg ctt ggt gtc tca agg cag ctc aga att 2369  
Gly Pro Arg Asp Arg Asp Trp Leu Gly Val Ser Arg Gln Leu Arg Ile  
25 30 35 40

aaa gca tgg aac aga cag ctg tat cca gag tgg aca gaa agc cag ggg 2417  
Page 18

SEQCRF05081156

Lys	Ala	Trp	Asn	Arg	Gln	Leu	Tyr	Pro	Glu	Trp	Thr	Glu	Ser	Gln	Gly		
			45						50					55			
cct	gac	tgc	tgg	aga	g	gtaggaactt	ggcaatttcc	aggaggagata	tggtggaaat								2473
Pro	Asp	Cys	Trp	Arg													
			60														
gggtggggag	gggaacgggg	ttgaatgtac	ttaggaagat	agggaaggaa	aaggcataca												2533
gggaggagaa	gccaaggagc	taattaatgc	agctgccctt	ttcag	gt	ggc	cac	ata									2589
						Gly	Gly	His	Ile								65
tcc	ctg	aag	gtc	agc	aat	gat	ggg	cct	aca	ctg	att	ggg	gca	aat	gct		2637
Ser	Leu	Lys	Val	Ser	Asn	Asp	Gly	Pro	Thr	Leu	Ile	Gly	Ala	Asn	Ala		
				70					75					80			
tcc	ttc	tct	att	gcc	ttg	cac	ttt	cct	aaa	agc	caa	aag	gtg	ctg	cca		2685
Ser	Phe	Ser	Ile	Ala	Leu	His	Phe	Pro	Lys	Ser	Gln	Lys	Val	Leu	Pro		
			85					90					95				
gat	ggg	cag	gtc	atc	tgg	gcc	aac	aac	acc	atc	atc	aat	g	gtgagtacct			2735
Asp	Gly	Gln	Val	Ile	Trp	Ala	Asn	Asn	Thr	Ile	Ile	Asn					
		100					105					110					
ctccgcctcc	ttcccaaggt	ccagaatccc	tggtatcccc	aatgagctca	aggaatcctc												2795
ctcctctttt	tttttttttt	tttttacaaa	ttatatatgt	aacacatatt	cactgcagaa												2855
aaattagaaa	acacagataa	acaaaaaaga	aaaaaaatta	tagttcccca	aatggggcac												2915
agaagaccca	gtggacatag	aagttggata	gacttggatt	taaactgggt	accagtatgt												2975
gaccctggac	aagtcactga	attgttttgt	tcttccattc	ccttatctat	agaatgggga												3035
tgataacact	ttaaaagggt	cttgtaagga	ttaaaatgtg	ataatatata	aagatttttag												3095
cataatgcct	gccctgtgct	gtgcttagta	ccttagttta	gacgctttgc	aacccccatgg												3155
actgtagccc	accaggctcc	tctgtccatg	tggattctgc	aggcaagaat	actggagtgg												3215
gtcaccatgc	actcctccag	gggatcttcc	caactcaggg	atcgaaccca	ggtcctagcc												3275
tacagtatta	attgatgctg	ttattttttac	ttttatccca	ctagctagag	cacatcatcc												3335
tagacatttt	gatacatggc	ctaccaattt	gtgtccagtg	taagaatata	catgtgtgtg												3395
ctcagtggct	cagtcgtgtc	tgactctttg	caacccccatg	gactgtagcc	cgcgaaagct												3455
cctctgcccc	tgggattgcc	cagccaagaa	tactggagca	ggttgccatt	tcttcctcca												3515
ggggatcttt	caacacaggg	attgaatcct	tgtctcctgt	gtttcctgca	ttggcaggtg												3575
tattcttttac	caactgagcca	cctgggaaac	cccttaagta	tatacacata	aatctttttat												3635
agtttccatt	ctcccttcta	ccactccaaa	taggtttatac	caaggagaat	gtatttttgg												3695
agctaggcag	tattcctgga	gcccctctct	gggagtcattg	ttaaagggtt	tggtgtacag												3755
tgaggaatgc	cagggattga	gggagacttg	ctgtcttctt	ttcag	gg	agc	cag	gtg									3811
						Gly	Ser	Gln	Val								
tggtgga	gga	cag	ctg	gta	tat	ccc	caa	gaa	cct	gat	gat	acc	tgc	atc			3859
Trp	Gly	Gly	Gln	Leu	Val	Tyr	Pro	Gln	Glu	Pro	Asp	Asp	Thr	Cys	Ile		
115				120					125					130			
ttc	ccc	gat	ggg	gag	ccc	tgc	cct	tct	ggc	cct	cta	tct	cag	aaa	aga		3907
Phe	Pro	Asp	Gly	Glu	Pro	Cys	Pro	Ser	Gly	Pro	Leu	Ser	Gln	Lys	Arg		
			135						140					145			
tgc	ttt	gtt	tat	gtc	tgg	aag	acc	tgg	g	gtaagagttt	cccttctctg						3955
Cys	Phe	Val	Tyr	Val	Trp	Lys	Thr	Trp									
			150					155									
gcctgtcatt	cacacttaaa	ttcacttctt	cctacctgat	ccccttttctt	ttggtctcat												4015
ccttaaatcc	tgtgagtttc	cctaattctt	acttccccca	tgactccttc	ctcttccaca												4075
gcacctagtc	aactctatta	tacttctttc	tgggagccct	gctccaatta	tagtcccatc												4135
ccatggaccc	tctcataagg	actttttttc	tgcccaacat	atgcaagctt	aaactctctg												4195

SEQCRF05081156

aaataacccat ccttgataca tctcctgacc ttccttctct gggtccatct ctaaccctgc	4255
cccagtcctcc tttagaccagt aaccccccttc cctactcttc tttccaaaaa cctcag ac Asp	4313
caa tac tgg caa gtt ctg ggg ggc cca gtg tct gga ctg agc atc ggg Gln Tyr Trp Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly 160 165 170	4361
aca gac aag gca atg ctg ggc aca tat aac atg gaa gtg act gtc tac Thr Asp Lys Ala Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr 175 180 185	4409
cac cgc cgg ggg tcc cag agc tat gtg ccc ctc gct cac tcc agt tca His Arg Arg Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser 190 195 200	4457
gcc ttc acc att act g gtaaggactg aggagggggac aaggccagtt gcagggcagg Ala Phe Thr Ile Thr 205	4513
agaaggtggg gaggctgggc tggacaggaa aggggaaaga ggaaatggtg tgtaacctta caggggcaga accaggaaga tgtgggcaga gggatgtggg gcttgagacc cgtgaagggc caggcagctt ggggttggtt aaaaatatgg ctgtgaaaga agaagctgac agaaagaaga	4573 4633 4693
acttatgggtt ctcactttct ctgactccaa tcccag ac cag gtg ccc ttc tct Asp Gln Val Pro Phe Ser 210 215	4746
gtg agt gtg tct cag ctg cag gcc ttg gat gga agg aac aag cgc ttc Val Ser Val Ser Gln Leu Gln Ala Leu Asp Gly Arg Asn Lys Arg Phe 220 225 230	4794
ctg aga aag cag cct ctg acc ttt gcc ctc cag ctc cat gat ccc agt Leu Arg Lys Gln Pro Leu Thr Phe Ala Leu Gln Leu His Asp Pro Ser 235 240 245	4842
ggc tat ttg gct ggg gct gac ctt tcc tac acc tgg gac ttt ggt gac Gly Tyr Leu Ala Gly Ala Asp Leu Ser Tyr Thr Trp Asp Phe Gly Asp 250 255 260	4890
agt aca ggg acc ctg atc tct cgg gca ctc acg gtc act cac act tac Ser Thr Gly Thr Leu Ile Ser Arg Ala Leu Thr Val Thr His Thr Tyr 265 270 275	4938
cta gag tct ggc cca gtc act gca cag gtg gtg ctg cag gct gcc att Leu Glu Ser Gly Pro Val Thr Ala Gln Val Val Leu Gln Ala Ala Ile 280 285 290 295	4986
cct ctc acc tcc tgt ggc tcc tct cca gtt cca ggc act aca gat agg Pro Leu Thr Ser Cys Gly Ser Ser Pro Val Pro Gly Thr Thr Asp Arg 300 305 310	5034
cat gtg aca act gca gag gct cct gga acc aca gct ggc caa gtg cct His Val Thr Thr Ala Glu Ala Pro Gly Thr Thr Ala Gly Gln Val Pro 315 320 325	5082
act aca gaa gtc atg ggc acc aca cct ggc cag gtg cca act gca gag Thr Thr Glu Val Met Gly Thr Thr Pro Gly Gln Val Pro Thr Ala Glu 330 335 340	5130
gcc cct ggc acc aca gtt ggg tgg gtg cca acc aca gag gat gta ggt	5178

## SEQCRF05081156

Ala	Pro	Gly	Thr	Thr	Val	Gly	Trp	Val	Pro	Thr	Thr	Glu	Asp	Val	Gly		
345						350					355						
acc	aca	cct	gag	cag	gtg	gca	acc	tcc	aaa	gtc	tta	agt	aca	aca	cca	5226	
Thr	Thr	Pro	Glu	Gln	Val	Ala	Thr	Ser	Lys	Val	Leu	Ser	Thr	Thr	Pro		
360					365					370					375		
gtg	gag	atg	cca	act	gca	aaa	gct	aca	ggg	agg	aca	cct	gaa	gtg	tca	5274	
Val	Glu	Met	Pro	Thr	Ala	Lys	Ala	Thr	Gly	Arg	Thr	Pro	Glu	Val	Ser		
				380					385					390			
act	aca	gag	ccc	tct	gga	acc	aca	gtt	aca	cag	gga	aca	act	cca	gag	5322	
Thr	Thr	Glu	Pro	Ser	Gly	Thr	Thr	Val	Thr	Gln	Gly	Thr	Thr	Pro	Glu		
			395					400					405				
ctg	gtg	gag	acc	aca	gct	gga	gag	gtg	tcc	act	cct	gag	cct	gcg	ggg	5370	
Leu	Val	Glu	Thr	Thr	Ala	Gly	Glu	Val	Ser	Thr	Pro	Glu	Pro	Ala	Gly		
		410					415					420					
tca	aat	act	agc	tca	ttc	atg	cct	aca	gaa	ggg	act	gca	g	gta	aggggggc	5420	
Ser	Asn	Thr	Ser	Ser	Phe	Met	Pro	Thr	Glu	Gly	Thr	Ala					
425						430					435						
caccatgaat	gagttcatag	aggtggggca	tttgtcacag	ctctgaagac	ctgaaagaat	5480											
tgctcaggac	ccagatgtta	ctcaatcctt	agcttagcag	tgaggtcccc	tcagaatctt	5540											
cactggtttt	aaaaccccct	aagtccctct	taatggcaca	gaatagatcc	agagttcagg	5600											
aaaccagggg	cttctcctag	gccaggggta	gagagcttat	tctctcttcc	tgaagagaag	5660											
ttcaggaagc	agtgtgtgat	catttggtgg	tggtgtcag	tcatgtctga	ctctttgtga	5720											
cctcatggac	tatggcccac	caggctcctc	tgtccataga	attctccagg	caagaacact	5780											
ggagtgggtg	gccattttct	tctccagggg	atcttccctg	cccagggatt	aaacccgaat	5840											
tggcaggtgg	attcttttacc	cgagccacct	agaaagtccc	atgtgatcat	tagataatac	5900											
ttataacctca	ttttctgatt	aagtgtaaac	acagaaatct	ttctgacacc	acttcccacc	5960											
cctggattcc	catcccaaag	taggtttacc	tggaattgtg	gtaggaatac	taaaaaggga	6020											
gaagttagat	agtgaacta	tgacttaaca	catgtcaa	gtctgaccca	ggacctggca	6080											
cagtgtaggg	tgtgataaac	atttgggatg	tctaaaattc	tgactcta	cctgtgactc	6140											
tggggcagtc	atttctcttg	ggcctttctt	tatcttaaaa	aatgagagtt	tccagctctt	6200											
gtctgattct	aagcctggat	ccagtagctc	tgactctacc	tggaataatg	cttggtgggc	6260											
ctgttttcag	gttagtcatt	tgctttttga	cittgacctc	ttaatcctct	cctccag	6317											
gc	tcc	ctg	agt	ccc	ctg	ccg	gat	gac	act	gcc	acc	tta	gtc	ctg	gag	6364	
Gly	Ser	Leu	Ser	Pro	Leu	Pro	Asp	Asp	Thr	Ala	Thr	Leu	Val	Leu	Glu		
			440					445					450				
aag	cgc	caa	gcc	ccc	ctg	gat	tgt	gtt	ctg	tat	cgc	tat	ggc	tcc	ttt	6412	
Lys	Arg	Gln	Ala	Pro	Leu	Asp	Cys	Val	Leu	Tyr	Arg	Tyr	Gly	Ser	Phe		
		455					460					465					
tcc	ctc	acc	ctg	gac	att	gtc	c	gtg	agt	cttg	cct	acatt	gt	ccg	taagctg	6464	
Ser	Leu	Thr	Leu	Asp	Ile	Val											
		470				475											
gtggagggag	gcgtgtgctg	cttaggggtg	cccagtgga	gcacaccttg	gaaggaatta	6524											
ctcacctgga	caaggagaat	accagatcc	caggggtttc	atatgaaggc	agaatgggat	6584											
tagggaggca	gcccaggac	cttcctggcc	atgggccttg	ggggaggata	agtagaggag	6644											
tctcagactt	aaaaaaatct	tgcaactttg	cag	ag	ggg	att	gag	agt	gct	gag	6697						
			Gln	Gly	Ile	Glu	Ser	Ala	Glu								
						480											
atc	cta	cag	gct	gtg	tca	tcc	agt	gaa	gga	gat	gca	ttt	gag	ctg	act	6745	
Ile	Leu	Gln	Ala	Val	Ser	Ser	Ser	Glu	Gly	Asp	Ala	Phe	Glu	Leu	Thr		
		485					490						495				

SEQCRF05081156

gtg tct tgc caa ggc gg	gtgagtgtcc cacggttgcc ctgagaactc	6792
Val Ser Cys Gln Gly Gly		
500		
ctgggggtgac tgctgtcctg ttctctggtg tctagtgtcc cttcccagat tccctgacgt		6852
aagctgacat ctctcccag g	cta ccc aag gaa gcc tgc atg gac atc tca	6902
	Leu Pro Lys Glu Ala Cys Met Asp Ile Ser	
505	510	
tcg cca ggg tgt cag ctg cct gcc cag cgg ctg tgt cag cct gtg ccc		6950
Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu Cys Gln Pro Val Pro		
515	520 525 530	
ccc agc cca gcc tgc cag ctg gtt ttg cac cag gta ctg aag ggt ggc		6998
Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Val Leu Lys Gly Gly		
	535 540 545	
tca ggg acc tac tgc ctc aat gtg tct ttg gct gat gcc aat agc ctg		7046
Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Ala Asn Ser Leu		
	550 555 560	
gcg atg gtc agc acc cag ctt gtc atg cct g gtaggtagtt ggacaagagg		7097
Ala Met Val Ser Thr Gln Leu Val Met Pro		
565	570	
taggatgaag acacggggag atggtagagg ttacctacta gaggaagcag aactgaatg		7157
cagccgtatc tgggattcca cccatag gg	caa gaa gca ggc ctc agg cag gct	7210
	Gly Gln Glu Ala Gly Leu Arg Gln Ala	
	575 580	
cct ctg ttc gtg ggc atc ttg ctg gtg cta aca gct ttg ttg ctt gca		7258
Pro Leu Phe Val Gly Ile Leu Leu Val Leu Thr Ala Leu Leu Leu Ala		
	585 590 595	
tct ctg ata tac ag	gtgagatccc cgccatcctg ctcccactcc tttaccctt	7312
Ser Leu Ile Tyr Arg		
600		
attaccacca ccactcttcc tcatgggaag aagaaaccac caaccctttt gggaaagtgt		7372
agagtccaag aaagagccca gacttggaag ttcaacaggt ctaggctgca gtcttgctgg		7432
tgggaccctg gggaagtcca ttaacccttc tgagccactg aaaagtagga aacataatac		7492
ctgtcctgtg gggctgtttt cagggtctta gacaatgtga gtaaaacacc tggttctgaa		7552
acaaaagtgg aataaatgat gatctcaatg actgttgtta tgaataatat caacagtgga		7612
gaagaactca gtgaactgag ttctccacct gccagaaagg caaatcccta ggcctggagg		7672
gctgaggtcc tcaaagcagg gaagcctgta gggtagagagg gaaatgggtca gagcttacca		7732
taaacataag agaggataaa ccctgttggt gagaagagga gggagccagg atcaagacca		7792
agtcaacctg ggttatggtt tagtcttttt tttttagaga agcacaaaga ggttgccatt		7852
gaccaccact aaccagtatc cctgcttttc tcccaatatc		7892
ag g cga aga ctt atg aag caa ggc	tca gca gtc ccc ctt ccc cag	7937
Arg Arg Leu Met Lys Gln Gly	Ser Ala Val Pro Leu Pro Gln	
605	610 615	
ctg cca cac ggt aga acc cag tgg	cta cgt ctg ccc tgg gtc ttc cgc	7985
Leu Pro His Gly Arg Thr Gln Trp	Leu Arg Leu Pro Trp Val Phe Arg	
620	625 630	
tct tgc ccc att ggt gag agc aaa ccc ctc ctc agt gga cag cag gtc		8033
Ser Cys Pro Ile Gly Glu Ser	Lys Pro Leu Leu Ser Gly Gln Gln Val	
635	640 645	

tgagtgtctt tatgtgaagt catgatttac ccaggtggac agcaaggcct gtcttttctc 8093

tggtcttccc tcagagacta ccattgcctg aaataaagac tcagaacttg 8143

<210> 6  
 <211> 648  
 <212> PRT  
 <213> Bos taurus

<400> 6  
 Met Asp Leu Val Leu Arg Lys Tyr Leu Leu His Val Ala Leu Met Gly  
 1 5 10 15  
 Val Leu Ala Val Gly Thr Thr Glu Gly Pro Arg Asp Arg Asp Trp Leu  
 20 25 30  
 Gly Val Ser Arg Gln Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr  
 35 40 45  
 Pro Glu Trp Thr Glu Ser Gln Gly Pro Asp Cys Trp Arg Gly Gly His  
 50 55 60  
 Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala Asn  
 65 70 75 80  
 Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser Gln Lys Val Leu  
 85 90 95  
 Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile Ile Asn Gly Ser  
 100 105 110  
 Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro Asp Asp Thr  
 115 120 125  
 Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro Leu Ser Gln  
 130 135 140  
 Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp Asp Gln Tyr Trp Gln  
 145 150 155 160  
 Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Asp Lys Ala  
 165 170 175  
 Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr His Arg Arg Gly  
 180 185 190  
 Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr Ile  
 195 200 205  
 Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala Leu  
 210 215 220  
 Asp Gly Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe Ala  
 225 230 235 240  
 Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Gly Ala Asp Leu Ser  
 245 250 255  
 Tyr Thr Trp Asp Phe Gly Asp Ser Thr Gly Thr Leu Ile Ser Arg Ala  
 260 265 270  
 Leu Thr Val Thr His Thr Tyr Leu Glu Ser Gly Pro Val Thr Ala Gln

	275						280								285
Val	Val	Leu	Gln	Ala	Ala	Ile	Pro	Leu	Thr	Ser	Cys	Gly	Ser	Ser	Pro
	290					295					300				
Val	Pro	Gly	Thr	Thr	Asp	Arg	His	Val	Thr	Thr	Ala	Glu	Ala	Pro	Gly
305					310					315					320
Thr	Thr	Ala	Gly	Gln	Val	Pro	Thr	Thr	Glu	Val	Met	Gly	Thr	Thr	Pro
				325					330					335	
Gly	Gln	Val	Pro	Thr	Ala	Glu	Ala	Pro	Gly	Thr	Thr	Val	Gly	Trp	Val
			340					345					350		
Pro	Thr	Thr	Glu	Asp	Val	Gly	Thr	Thr	Pro	Glu	Gln	Val	Ala	Thr	Ser
		355					360					365			
Lys	Val	Leu	Ser	Thr	Thr	Pro	Val	Glu	Met	Pro	Thr	Ala	Lys	Ala	Thr
	370					375					380				
Gly	Arg	Thr	Pro	Glu	Val	Ser	Thr	Thr	Glu	Pro	Ser	Gly	Thr	Thr	Val
385					390					395					400
Thr	Gln	Gly	Thr	Thr	Pro	Glu	Leu	Val	Glu	Thr	Thr	Ala	Gly	Glu	Val
				405					410					415	
Ser	Thr	Pro	Glu	Pro	Ala	Gly	Ser	Asn	Thr	Ser	Ser	Phe	Met	Pro	Thr
			420					425					430		
Glu	Gly	Thr	Ala	Gly	Ser	Leu	Ser	Pro	Leu	Pro	Asp	Asp	Thr	Ala	Thr
		435					440					445			
Leu	Val	Leu	Glu	Lys	Arg	Gln	Ala	Pro	Leu	Asp	Cys	Val	Leu	Tyr	Arg
	450					455					460				
Tyr	Gly	Ser	Phe	Ser	Leu	Thr	Leu	Asp	Ile	Val	Gln	Gly	Ile	Glu	Ser
465					470					475					480
Ala	Glu	Ile	Leu	Gln	Ala	Val	Ser	Ser	Ser	Glu	Gly	Asp	Ala	Phe	Glu
				485					490					495	
Leu	Thr	Val	Ser	Cys	Gln	Gly	Gly	Leu	Pro	Lys	Glu	Ala	Cys	Met	Asp
			500					505					510		
Ile	Ser	Ser	Pro	Gly	Cys	Gln	Leu	Pro	Ala	Gln	Arg	Leu	Cys	Gln	Pro
		515					520					525			
Val	Pro	Pro	Ser	Pro	Ala	Cys	Gln	Leu	Val	Leu	His	Gln	Val	Leu	Lys
	530					535					540				
Gly	Gly	Ser	Gly	Thr	Tyr	Cys	Leu	Asn	Val	Ser	Leu	Ala	Asp	Ala	Asn
545					550					555					560
Ser	Leu	Ala	Met	Val	Ser	Thr	Gln	Leu	Val	Met	Pro	Gly	Gln	Glu	Ala
			565						570					575	
Gly	Leu	Arg	Gln	Ala	Pro	Leu	Phe	Val	Gly	Ile	Leu	Leu	Val	Leu	Thr
			580					585					590		
Ala	Leu	Leu	Leu	Ala	Ser	Leu	Ile	Tyr	Arg	Arg	Arg	Leu	Met	Lys	Gln
	595						600					605			
Gly	Ser	Ala	Val	Pro	Leu	Pro	Gln	Leu	Pro	His	Gly	Arg	Thr	Gln	Trp



620

Leu Arg Leu Pro Trp Val Phe Arg Ser Cys Pro Ile Gly Glu Ser Lys  
625 630 635 640

Pro Leu Leu Ser Gly Gln Gln Val  
645

<210>	7
<211>	294
<212>	DNA
<213>	Artificial sequence

<220>  
<223> Probe

<400>	7						
gttgctggaa	ggaagaacag	gatggatctg	gtgctgagaa	aataccttct	ccatgtggct		60
ctgatgggtg	ttcttctggc	tgtagggacc	acagaagggtg	agtgtgggat	gttggacatg		120
aacaagtgtg	aatttggggg	tgcacacctg	ctctggtttt	tctctcccta	aaatggaaga		180
tatcagttagt	gcttcagggtg	tctcccaccc	atttgattta	gtgaggacat	gggcaactga		240
gctccctccc	cacatgaaga	tttgggtqca	tgtgtattca	ggcactttggg	actg		294

<210>	8
<211>	294
<212>	DNA
<213>	Artificial sequence

<220>  
<223> Probe

<400>	8						
gttgctggaa	ggaagaacag	gatggatctg	gtgctgagaa	aataccttct	ccatgtggct		60
ctgatgggtg	ttcttctggc	tgtaaggacc	acagaagggtg	agtgtgggat	gttggacatg		120
aacaagtgtg	aattttgggtg	tgcacacctg	ctctggtttt	tctctcccta	aaatggaaga		180
tatcagtagt	gcttcagggtg	tctcccaccc	atttgattta	gtgaggacat	gggcaactga		240
gctccctccc	gcatcatgaaga	tttgggtgca	tgtgtgttca	ggcaccttggg	actg		294

<210>	9
<211>	291
<212>	DNA
<213>	Artificial sequence

<220>  
<223> Probe

<400>	9						
gttgctggaa	ggaagaacag	gatggatctg	gtgctgagaa	aataccttct	ccatgtggct		60
ctgatgggtg	tcttggctgt	agggaccaca	gaaggtgagt	gtgggatgtt	ggacatgaac		120
aagtgtgaat	ttgggggttg	acacctgctc	tggtttttct	ctccctaaaa	tggaagatat		180
cagtagtgtc	tcagggtgtc	cccacctcatt	tgatttagtg	aggacatggg	caactgagct		240
ccctcccccac	atgaagctatt	gggtgcattgt	gtgttcaggc	acttgggact	g		291

<210>	10
<211>	30
<212>	DNA
<213>	Artificial sequence

$\langle 220 \rangle$

&lt;223&gt; Synthetic Primer

&lt;400&gt; 10

gttgctggaa ggaagaacag gatggatctg

30

&lt;210&gt; 11

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Synthetic Primer

&lt;400&gt; 11

cagtcccaag tgcctgaaca cacatgcacc

30

&lt;210&gt; 12

&lt;211&gt; 2086

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Synthetic Nucleotide

&lt;400&gt; 12

ggctctttggt	tgctggaagg	aagaacagga	tggatctggt	gctgagaaaa	tacctttctcc	60
atgtggctct	gatgggtggt	cttctggctg	taaggaccac	agaaggaccc	agagacaggg	120
actggcttgg	tgtctcaagg	cagctcagaa	ttaaagcatg	gaacagacag	ctgtatccag	180
agtggacaga	aagccagggg	cctgactgct	ggagaggttg	ccacatatcc	ctgaagggtca	240
gcaatgatgg	gcctacactg	attggggcaa	atgcttccct	ctctattgcc	ttgcactttc	300
ctaaaagcca	aaaggtgctg	ccagatgggc	aggtcatctg	ggccaacaac	accatcatca	360
atgggagcca	ggtgtgggga	ggacagctgg	tatatcccca	agaacctgat	gataacctgca	420
tcttccccga	tggggagccc	tgcccttctg	gccctctatc	tcagaaaaga	tgctttgttt	480
atgtctggaa	gacctgggac	caatactggc	aagttctggg	gggcccagtg	tctggactga	540
gcatcgggac	agacaaggca	atgctgggca	catataacat	ggaagtgact	gtctaccacc	600
gccgggggtc	ccagagctat	gtgcccctcg	ctcactccag	ttcagccttc	accattactg	660
accaggtgcc	cttctctgtg	agtgtgtctc	agctgcaggc	cttggatgga	aggaacaagc	720
gcttcctgag	aaagcagcct	ctgacctttg	ccctccagct	ccatgatccc	agtggctatt	780
tggctggggc	tgacctttcc	tacacctggg	actttggtga	cagtacaggg	accctgatct	840
ctcgggcact	cacggtcact	cacacttacc	tagagtctgg	cccagtcact	gcacaggttg	900
tgctgcaggc	tgccattcct	ctcacctcct	gtggctcctc	tccagttcca	ggcactacag	960
ataggcatgt	gacaactgca	gaggctcctg	gaaccacagc	tggccaagtg	cctactacag	1020
aagtcattgg	caccacacct	ggccaggtgc	caactgcaga	ggcccctggc	accacagttg	1080
ggtgggtgcc	aaccacagag	gatgtaggta	ccacacctga	gcaggtggca	acctccaaag	1140
tcttaagtac	aacaccagtg	gagatgccaa	ctgcaaaagc	tacaggtagg	acacctgaag	1200
tgtcaactac	agagccctct	ggaaccacag	ttacacaggg	aacaactcca	gagctggttg	1260
agaccacagc	tggagaggtg	tccactcctg	agcctgcggg	ttcaaatact	agctcattca	1320
tgccctacaga	aggtactgca	ggctcccctga	gtcccctgcc	ggatgacact	gccaccttag	1380
tcctggagaa	gcgccaagcc	cccctggatt	gtgttctgta	tcgctatggc	tccttttccc	1440
tcaccctgga	cattgtccag	ggtattgaga	gtgctgagat	cctacaggct	gtgtcatcca	1500
gtgaaggaga	tgcatttgag	ctgactgtgt	cttgccaagg	cgggctaccc	aaggaagcct	1560
gcatggacat	ctcatcgcca	gggtgtcagc	tgcctgcccc	gcggctgtgt	cagcctgtgc	1620
ccccagcccc	agcctgccag	ctggtttttg	accaggtact	gaaggggtgg	tcagggacct	1680
actgcctcaa	tgtgtctttg	gctgatgcca	atagcctggc	gatggtcagc	acccagcttg	1740
tcattgcctg	gcaagaagca	ggcctcaggc	aggctcctct	gttcgtgggc	atcttgctgg	1800
tgctaacagc	tttgttgctt	gcatctctga	tatacaggcg	aagacttatg	aagcaaggct	1860
cagcagtcct	ccttccccag	ctgccacacg	gtagaaccca	gtggctacgt	ctgccctggg	1920
tcttccgctc	ttgccccatt	ggtgagagca	aaccctcctc	cagtggacag	caggtctgag	1980
tgctcttatg	tgaagtcatt	atttaccacg	gtggacagca	aggcctgtct	tttctctggt	2040
cttccctcag	agactaccat	tgccctgaaat	aaagactcag	aacttg		2086

SEQCRF05081156

<210> 13  
 <211> 649  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Synthetic peptide

<400> 13  
 Met Asp Leu Val Leu Arg Lys Tyr Leu Leu His Val Ala Leu Met Gly  
 1 5 10 15

Val Leu Leu Ala Val Arg Thr Thr Glu Gly Pro Arg Asp Arg Asp Trp  
 20 25 30

Leu Gly Val Ser Arg Gln Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu  
 35 40 45

Tyr Pro Glu Trp Thr Glu Ser Gln Gly Pro Asp Cys Trp Arg Gly Gly  
 50 55 60

His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala  
 65 70 75 80

Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser Gln Lys Val  
 85 90 95

Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile Ile Asn Gly  
 100 105 110

Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro Asp Asp  
 115 120 125

Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro Leu Ser  
 130 135 140

Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp Asp Gln Tyr Trp  
 145 150 155 160

Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Asp Lys  
 165 170 175

Ala Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr His Arg Arg  
 180 185 190

Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr  
 195 200 205

Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala  
 Page 27

210

215

Leu Asp Gly Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe  
225 230 235 240

Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Gly Ala Asp Leu  
245 250 255

Ser Tyr Thr Trp Asp Phe Gly Asp Ser Thr Gly Thr Leu Ile Ser Arg  
260 265 270

Ala Leu Thr Val Thr His Thr Tyr Leu Glu Ser Gly Pro Val Thr Ala  
275 280 285

Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser  
290 295 300

Pro Val Pro Gly Thr Thr Asp Arg His Val Thr Thr Ala Glu Ala Pro  
305 310 315 320

Gly Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Met Gly Thr Thr  
325 330 335

Pro Gly Gln Val Pro Thr Ala Glu Ala Pro Gly Thr Thr Val Gly Trp  
340 345 350

Val Pro Thr Thr Glu Asp Val Gly Thr Thr Pro Glu Gln Val Ala Thr  
355 360 365

Ser Lys Val Leu Ser Thr Thr Pro Val Glu Met Pro Thr Ala Lys Ala  
370 375 380

Thr Gly Arg Thr Pro Glu Val Ser Thr Thr Glu Pro Ser Gly Thr Thr  
385 390 395 400

Val Thr Gln Gly Thr Thr Pro Glu Leu Val Glu Thr Thr Ala Gly Glu  
405 410 415

Val Ser Thr Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser Phe Met Pro  
420 425 430

Thr Glu Gly Thr Ala Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala  
435 440 445

Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr  
450 455 460

SEQCRF05081156

Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val Gln Gly Ile Glu  
465 470 475 480

Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly Asp Ala Phe  
485 490 495

Glu Leu Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met  
500 505 510

Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu Cys Gln  
515 520 525

Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Val Leu  
530 535 540

Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Ala  
545 550 555 560

Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro Gly Gln Glu  
565 570 575

Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu Val Leu  
580 585 590

Thr Ala Leu Leu Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys  
595 600 605

Gln Gly Ser Ala Val Pro Leu Pro Gln Leu Pro His Gly Arg Thr Gln  
610 615 620

Trp Leu Arg Leu Pro Trp Val Phe Arg Ser Cys Pro Ile Gly Glu Ser  
625 630 635 640

Lys Pro Leu Leu Ser Gly Gln Gln Val  
645

<210> 14  
<211> 8138  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic nucleotide

<400> 14	
gttgctggaa ggaagaacag gatggatctg gtgctgagaa aataccttct ccatgtggct	60
ctgatgggtg ttcttctggc tgtaaggacc acagaagggt agtgtgggat gttggacatg	120
aacaagtgtg aatttggggt tgcacacctg ctctggtttt tctctcccta aaatggaaga	180
tatcagtagt gcttcagggt tctccacacc atttgattta gtgaggacat gggcaactga	240
gctccctccc cacatgaaga tttgggtgca tgtgtgttca ggcacttggg actgaacctg	300
aaaacaaccc catctacctg gatgggtgag agaacagtat gtctccgtgg ccctaatttt	360

## SEQCRF05081156

gagatgctct	gaatagtgag	ctggaacatg	ggtgccaagg	tagtaaaatg	agtggaaact	420
catttaggct	ttgtctcagg	cacttgggat	aggggtattta	ggagatagag	aaagatagga	480
gataggagaa	aggagaaaga	ggatgtggta	ttggatagaa	gggtaatgag	gcacctcatc	540
ccctcttttg	gatgggcatg	ggtgaacaca	gcccaggctt	ttgttctggg	gctggaagag	600
acaggcagaa	gggtctcagc	tgagcatcac	atgaaagggc	tctgggggat	tggggcctcg	660
tgacaggagc	aaggcggtg	gggtggggat	ggtgagaggg	tctggaatgt	cccgtgctgc	720
tctgaggagg	gaggattggg	agtggagaaa	gaatggggca	tcttatgatt	ctcttgttct	780
tgtggtgagg	tattcagtg	gataattcta	gatcctcccc	caagagaatc	aaccagggtt	840
ctggtacatg	ttagagatgg	agtgaggata	gtctgtgatg	tgcaaaaata	tctacattgt	900
acccagtg	cccctttctc	tagatccctg	gtctcacaga	cttcttggaa	cttctccttg	960
atctgacttc	cctcattcat	ggtgtcattt	caagtcttat	tcttttacta	tgttcgttat	1020
tgtattcttg	aaatatcctg	ttcatatgtg	tccacccaag	gctcttaata	tgttgtgctt	1080
acttttttgg	tccagatttt	taaaatcata	agaagacatt	tttatatagt	tcatgaaatt	1140
ttgcatggac	tgagtttgat	aattttgttt	agtgtgaatt	aacatttgtt	ttatttaaga	1200
aaaaaaaaata	tttttttaca	gaaacctact	gaattttagt	ggtttttaaaa	taacatgatg	1260
tctgggattt	gcttttgaat	gcttcagcca	aaaaacaac	gaacaacaaa	aataaaggat	1320
agataaagca	aatgtgacaa	aatgctgata	gttgttggac	cttggggaga	cacatgcaga	1380
gccatcacat	cacttttttt	cagacatctt	tcttggtcag	ttataatcat	tttgtttgtc	1440
cccactccca	atttctactt	gcctctagtc	catcctcctc	actgcttgcc	aaagtgatcc	1500
ttctaaaaca	caaattctgat	catattcaaa	aagcttttga	agggtaagtt	ttatgggtata	1560
tgctaatatg	cagtacaaca	aacaaaatcg	tctgaggtgc	cgttgcctac	aggataaagt	1620
ccaaactcct	ttgcctggca	ctccaagccc	ccactctatc	ttcttggcct	catctctcat	1680
gatgtacatc	agccacattg	ctagtgtctg	ctcatggcct	tctgcctaga	atgctttatg	1740
ccccagccaa	ctattttactg	tcttcttcag	tcgaccagag	tgcaatttac	ctgtttaaaa	1800
tctatcattt	tgttatacat	tgtgcatgtc	tattatggct	catattaagc	aatgccttgg	1860
attatagtaa	tttatgtata	tgtctatttc	atatacttta	acctgaacct	cttcagaacc	1920
atttcttttt	catttcttaa	gttcttttga	cctagcccag	tgcttggtag	gtcgtgggta	1980
ttcagtagat	taaaatgcac	tttaagggaac	ttcccttggt	gtccatcaag	tggctaaggc	2040
tctgtgtctc	caatgcaggg	gaccagggtt	caatctcagg	tcagggaact	agatcccaca	2100
ggtcacaact	aagagtttgc	aagccacaac	tacctgacct	cacatgccac	aactaatcga	2160
agatccctcg	tgctgcaact	aagtcctagt	gcagttaaat	atattttttt	aatgcacttt	2220
gaatgtgaga	atgaatgatg	tgtcacagac	actgttgtcc	cctgagaagg	gagtgaagta	2280
tgatttgagg	gcccctcatg	tatatcttcc	tttttaggac	ccagagacag	ggactggctt	2340
ggtgtctcaa	ggcagctcag	aattaaagca	tggaacagac	agctgtatcc	agagtggaca	2400
gaaagccagg	ggcctgactg	ctggagaggt	aggaacttgg	caatttccag	ggaggatatg	2460
gtggaaatgg	gtggggaggg	gaacgggggt	gaatgtactt	aggaagatag	ggaaggaaaa	2520
ggcatacagg	gaggagaagc	caaggagcta	attaatgcag	ctgccctttt	caggtggcca	2580
catatccctg	aaggtcagca	atgatgggcc	tacactgatt	ggggcaaatg	cttcccttct	2640
tattgccttg	cacttttcta	aaagccaaaa	ggtgctggca	gatgggcagg	tcacttgggc	2700
caacaacacc	atcatcaatg	gtgagtacct	ctccgcctcc	ttcccaagg	ccagaatccc	2760
tggtatcccc	aatgagctca	aggaatcctc	ctcctctttt	tttttttttt	tttttaca	2820
ttatatatgt	aacacatatt	cactgcagaa	aaattagaaa	acacagataa	acaaaaaga	2880
aaaaaaaaatta	tagttcccca	aatggggcac	agaagaccca	gtggacatag	aagttggata	2940
gacttggatt	taaactgggt	accagtatgt	gaccttgagc	aagtcactga	attgttttgt	3000
tcttccattc	ctttatctat	agaatgggga	tgataacact	ttaaaagggt	cttgtaagga	3060
ttaaaatgtg	ataatatata	aagatttttag	cataatgcct	gccctgtgct	gtgcttagta	3120
ccttagttta	gacgctttgc	aaccccatgg	actgtagccc	accaggctcc	tctgtccatg	3180
tggtattctg	aggcaagaat	actggagtg	gtcaccatgc	actcctccag	gggatcttcc	3240
caactcagg	atcgaaccca	ggtcctagcc	tacagtatta	attgatgctg	ttattttttac	3300
ttttatccca	ctagctagag	cacatcatcc	tagacatttt	gatacatggc	ctaccaattt	3360
gtgtccagtg	taagaatata	catgtgtgtg	ctcagtggct	cagtcgtgtc	tgactctttg	3420
caaccccatg	gactgtagcc	cgcgaaagct	cctctgccca	tgggattgcc	cagccaagaa	3480
tactggagca	ggttgccatt	tcttcttcca	ggggatcttt	caacacaggg	attgaatcct	3540
tgtctcctgt	gtttcctgca	ttggcaggtg	tattcttttac	cactgagcca	cctgggaaac	3600
cccttaagta	tatacacata	aatctttttat	agttttccatt	ctcccttcta	ccactccaaa	3660
taggtttata	caaggagaat	gtatttttgt	agctaggcag	tattcctgga	gccccctctt	3720
gggagtcatg	ttaaagggtt	tggtgtacag	tgaggaaatgc	cagggattga	gggagacttg	3780
ctgtcttctt	ttcaggggagc	caggtgtggg	gaggacagct	ggtatatccc	caagaacctg	3840
atgatacctg	catcttcccc	gatggggagc	cctgcccttc	tggccctcta	tctcagaaaa	3900
gatgctttgt	ttatgtcttg	aagacctggg	gtaagagttt	cccttctctg	gcctgtcatt	3960
cacacttaaa	ttcaattctt	cctacctgat	cccccttctt	ttggtctcat	ccttaaatcc	4020
tgtgagtttc	cctaactctt	acttccccca	tgactccttc	ctcttccaca	gcacctagtc	4080
aactctatta	tacttctttc	tgggagccct	gctccaatta	tagtcccatc	ccatggacct	4140

## SEQCRF05081156

tctcataagg	actttttttcc	tgcccaacat	atgcaagctt	aaactctctg	aaataaccat	4200
ccttgataca	tctcctgacc	ttcctttctt	ggtttccatct	ctaaccctgc	cccagttctcc	4260
tttgaccagt	aacccccctt	cctactcttc	tttccaaaaa	cctcagacca	atactggcaa	4320
gttctggggg	gcccagtgtc	tggactgagc	atcgggacag	acaaggcaat	gctgggcaca	4380
tataacatgg	aagtgactgt	ctaccaccgc	cgggggtccc	agagctatgt	gccccctcgt	4440
cactccagtt	cagccttcac	cattactggt	aaggactgag	gaggggacaa	ggccagttgc	4500
agggcaggag	aaggtgggga	ggctgggctg	gacaggaaa	gggaaagagg	aaatggtgtg	4560
taaccttaca	ggggcagaac	caggaagatg	tgggcagagg	gatgtggggc	ttggagcccg	4620
tgaagggcca	ggcagcttgg	gttggttgaa	aaatatggct	gtgaaagaag	aagctgacag	4680
aaagaagaac	ttatggttct	cacttttctt	gactccaatc	ccagaccagg	tgcccttctc	4740
tgtgagtgtg	tctcagctgc	aggccttgga	tggaaaggaa	aagcgcttcc	tgagaaagca	4800
gcctctgacc	tttgccctcc	agctccatga	tcccagtggt	tattttggctg	gggctgacct	4860
ttcctacacc	tgggactttg	gtgacagtac	agggaccctg	atctctcggg	cactcacggg	4920
cactcacact	tacctagagt	ctggcccagt	cactgcacag	gtggtgctgc	aggctgccat	4980
tctctctacc	tctgtggct	cctctccagt	tccaggcact	acagataggc	atgtgacaa	5040
tgcagaggct	ccttggaacca	cagctggcca	agtgcctact	acagaagtca	tgggcaccac	5100
acctggccag	gtgccaactg	cagaggcccc	tggcaccaca	gttgggtggg	tgccaaccac	5160
agaggatgta	ggtaccacac	ctgagcagg	ggcaacctcc	aaagtcttaa	gtacaacacc	5220
agtggagatg	ccaactgcaa	aagctacagg	taggacacct	gaagtgtcaa	ctacagagcc	5280
ctctggaacc	acagttacac	agggaaaca	tccagagctg	gtggagacca	cagctggaga	5340
ggtgtccact	cctgagcctg	cgggttcaaa	tactagctca	ttcatgccta	cagaaggtga	5400
tgtgagtaag	ggggccacca	tgaatgagtt	catagaggtg	gggcattttgt	cacagctctg	5460
aagacctgaa	agaattgtct	aggaccacga	tgttactcaa	tccttagctt	agcagtggag	5520
ttccctcaga	atcttctact	gttttaaaac	cccctaagtc	cctcttaatg	gcacagaata	5580
gatccagagt	tcaggaaacc	agggctcttct	cctaggccag	gggtagagag	cttatttctct	5640
cttcttgaag	agaagttcag	gaagcagttg	gtgatcattt	ggtgggtggg	ctcagtcattg	5700
tctgactctt	tgtgacctca	tggactatgg	cccaccaggc	tcctctgtcc	atagaattct	5760
ccaggcaaga	acactggagt	gggtggccat	ttccttctcc	aggggatttt	ccctgccccag	5820
ggattaaacc	cgaattggca	ggtggattct	ttaccggagc	cacctagaaa	gtcccattgtg	5880
atcattagat	aatacttata	cctcattttc	tgattaagtg	taaacacaga	aatctttctg	5940
acaccacttc	ccacccctgg	attcccatcc	caaagtaggt	ttacctggaa	ttgtggtagg	6000
aataactaaa	agggagaagt	gagatagtga	cactatgact	taacacatgt	caaagtctctg	6060
accagagacc	tggcacagtg	tagggtgtga	taaacatttg	ggatgtctaa	aattctgact	6120
ctaaccctgt	gactctgggg	cagtcatttc	tcttgggcct	ttctttatct	taaaaaatga	6180
gagtttccag	ctcttgctctg	attctaagcc	tggatccagt	agctctgact	ctacctggaa	6240
aaatgcttgt	tgggcctgtt	ttcagggttag	tcatttgctt	tttgactttg	cctctttaat	6300
cctctcctcc	aggtctccctg	agtcctctgc	cggatgacac	tgccacctta	gtcctggaga	6360
agcgccaagg	ccccctggat	tgtgttctgt	atcgctatgg	ctccttttcc	ctcaccctgg	6420
acattgtccg	tgagctttgc	ctacattgtc	cgtaagctgg	tggaggagg	cgtgtgctgt	6480
ttagggttgc	ccagtggaa	cacaccttgg	aaggaattac	tcacctggac	aaggagaata	6540
cccagatccc	aggggtttca	tatgaaggca	gaatgggatt	agggaggcag	cccaggacc	6600
ttcctggcca	tgggccttgg	gggaggataa	gtagaggagt	ctcagactta	aaaaaatctt	6660
gcaactttgc	agagggtatt	gagagtgtctg	agatcctaca	ggctgtgtca	tccagtgaag	6720
gagatgcatt	tgagctgact	gtgtcttgcc	aaggcgggtg	agtgtcccac	ggttgccctg	6780
agaactcctg	gggtgactgc	tgtcctgttc	tctggtgtct	agtgtccctt	cccagattcc	6840
ctgacgtaag	ctgacatctc	tcccaggcta	cccaagggaag	cctgcatgga	catctcatcg	6900
ccagggtgtc	agctgcctgc	ccagcggctg	tgtcagcctg	tgccccccag	cccagcctgc	6960
cagctgggtt	tgcaccaggt	actgaagggt	ggctcaggga	cctactgcct	caatgtgtct	7020
ttggctgatg	ccaatagcct	ggcgtaggct	agcaccagc	ttgtcatgcc	tggtaggtag	7080
ttggacaaga	ggtaggatga	agacacgggg	agatggtaga	ggttacctac	tagaggaagc	7140
agacactgaa	tgcagccgta	tctgggattc	cacccatagg	gcaagaagca	ggcctcaggc	7200
aggctcctct	gttcgtgggc	atcttgctgg	tgctaacagc	tttgttgctt	gcatctctga	7260
tatacagggtg	agatccccgc	catcctgtct	ccactccttt	accccttatt	accaccacca	7320
ctcttctctca	tgggaagaag	aaaccaccaa	cccctttggg	aaagtgtaga	gtccaagaaa	7380
gagcccagac	ttggaagttc	aacagggtcta	ggctgcagtc	ttgctggtgg	gaccctgggg	7440
aagtccattta	accccttctga	gccactgaaa	agtaggaatc	ataatactctg	tcctgtgggg	7500
ctgtttttcag	ggctctagac	aatgtgagta	aaacacctgg	ttctgaaaca	aaagtggaa	7560
aaatgatgat	ctcaatgact	gttggttatga	ataatatcaa	cagtggagaa	gaactcagtg	7620
aactgagttc	tccacctgcc	agaaaggcaa	atccctaggc	ctggagggtc	gaggtcctca	7680
aagcagggaa	gcctgtaggg	tgagagggaa	atggtcagag	cttaccataa	acataagaga	7740
ggataaacc	tgttggttag	aagaggaggg	agccaggatc	aagaccaagt	caacctgggt	7800
tatggttttag	tctttttttt	ttagagaagc	acaaagaggt	tgccattgac	caccactaac	7860
cagtatccct	gctttttctc	caatatcagg	cgaagactta	tgaagcaagg	ctcagcagtc	7920

					SEQCRF05081156	
cccccttcccc	agctgccaca	cggtagaacc	cagtggctac	gtctgccctg	ggtctttccgc	7980
tcttgcccca	ttggtgagag	caaaccctc	ctcagtggac	agcaggtctg	agtgtcttta	8040
tgtgaagtca	tgatttacc	aggtggacag	caaggcctgt	cttttctctg	gtcttccctc	8100
agagactacc	attgcctgaa	ataaagactc	agaacttg			8138

<210> 15  
 <211> 2086  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic nucleotide

					<400> 15	
ggtcttttgg	tgctggaagg	aagaacagga	tggatctgg	gctgagaaaa	tacctttctcc	60
atgtggctct	gatgggtgtt	cttctggctg	taaggaccac	agaaggaccc	agagacaggg	120
actggcttgg	tgtctcaagg	cagctcagaa	ttaaagcatg	gaacagacag	ctgtatccag	180
agtggacaga	aagccagggg	cctgactgct	ggagaggttg	ccacatatcc	ctgaagggtca	240
gcaatgatgg	gcctacactg	attggggcaa	atgctttcct	ctctattggc	ttgcactttc	300
ctaaaagcca	aaaggtgctg	ccagatgggc	aggtcatctg	ggccaacaac	accatcatca	360
atgggagcca	ggtgtgggga	ggacagctgg	tatatcccca	agaacctgat	gatacctgca	420
tcttccccga	tggggagccc	tgcccttctg	gccctctatc	tcagaaaaga	tgctttgttt	480
atgtctggaa	gacctgggac	caatactggc	aagttctggg	gggcccagtg	tctggactga	540
gcatcgggac	agacaaggca	atgctgggca	catataacat	ggaagtgact	gtctaccacc	600
gccgggggtc	ccagagctat	gtgcccctcg	ctcactccag	ttcagccttc	accattactg	660
accaggtgcc	cttctctgtg	agtgtgtctc	agctgcaggc	cttggatgga	aggaacaagc	720
gcttcctgag	aaagcagcct	ctgacctttg	ccctccagct	ccatgatccc	agtggctatt	780
tggctggggc	tgacctttcc	tacacctggg	actttgggtg	cagtacaggg	accctgatct	840
ctcgggcact	cacggctact	cacacttacc	tagagtctgg	cccagtcact	gcacaggtgg	900
tgctgcaggc	tgccatttct	ctcacctcct	gtggctcctc	tccagttcca	ggcactacag	960
ataggcatgt	gacaactgca	gaggctcctg	gaaccacagc	tggccaaagt	cctactacag	1020
aagtcatggg	caccacacct	ggccaggtgc	caactgcaga	ggcccctggc	accacagttg	1080
ggtgggtgcc	aaccacagag	gatgtaggta	ccacacctga	gcaggtggca	acctccaaag	1140
tcttaagtac	aacaccagtg	gagatgccaa	ctgcaaaagc	tacaggtagg	acacctgaag	1200
tgtcaactac	agagccctct	ggaaccacag	ttacacaggg	aacaactcca	gagctgggtg	1260
agaccacagc	tggagaggtg	tccactcctg	agcctgcggg	ttcaaatact	agctcattca	1320
tgcttacaga	aggtactgca	ggctcccctg	gtcccctgcc	ggatgacact	gccaccttag	1380
tcctggagaa	gcgccaagcc	cccctggatt	gtgttctgta	tcgctatggc	tccttttccc	1440
tcaccctgga	cattgtccag	ggtattgaga	gtgctgagat	cctacaggct	gtgtcatcca	1500
gtgaaggaga	tgcattttag	ctgactgtgt	cttgccaagg	cgggctaccc	aaggaagcct	1560
gcatggacat	ctcatcgcca	gggtgtcagc	tgcctgcca	gcggctgtgt	cagcctgtgc	1620
ccccagccc	agcctgccag	ctggttttgc	accaggtact	gaaggggtgg	tcagggacct	1680
actgcctcaa	tgtgtctttg	gctgatgcca	atagcctggc	gatggtcagc	accagcttg	1740
tcatgcctgg	gcaagaagca	ggcctcaggc	aggctcctct	gttcgtgggc	atcttgctgg	1800
tgctaacagc	tttgttgctt	gcatctctga	tatacaggcg	aagacttatg	aagcaaggct	1860
cagcagtcct	ccttccccag	ctgccacacg	gtagaacca	gtggctacgt	ctgccctggg	1920
tcttccgctc	ttgccccatt	ggtgagagca	aaccctcct	cagtggacag	caggtctgag	1980
tgctcttatg	tgaagtcatt	atttaccacg	gtggacagca	aggcctgtct	tttctctgg	2040
cttccctcag	agactaccat	tgcttgaaat	aaagactcag	aacttg		2086

<210> 16  
 <211> 1584  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic nucleotide

					<400> 16	
ccaatactgg	caagttctgg	ggggcccagt	gtctggactg	agcatcggga	cagacaaggc	60
aatgctgggc	acataataca	tggaagtgc	tgtctaccac	cgccgggggt	cccagagcta	120



SEQCRF05081156

tgtgcccctc	gctcactcca	gttcagcctt	caccattact	gaccaggtgc	ccttctctgt	180
gagtgtgtct	cagctgcagg	ccttggatgg	aaggaacaag	cgcttcctga	gaaagcagcc	240
tctgaccttt	gccctccagc	tccatgatcc	cagtggctat	ttggctgggg	ctgacctttc	300
ctacacctgg	gacttttggtg	acagtacagg	gacctgatc	tctcgggcac	tcacggtcac	360
tcacacttac	ctagagtctg	gcccagtcac	tgcacaggtg	gtgctgcagg	ctgccattcc	420
tctcacctcc	tgtggctcct	ctccagttcc	aggcactaca	gataggcatg	tgacaactgc	480
agaggctcct	ggaaccacag	ctggccaagt	gcctactaca	gaagtcatgg	gcaccacacc	540
tggccaggtg	ccaactgcag	aggccccctg	caccacagtt	gggtgggtgc	caaccacaga	600
ggatgtaggt	accacacctg	agcaggtggc	aacctccaaa	gtcttaagta	caacaccagt	660
ggagatgcca	actgcaaaaag	ctacaggtag	gacacctgaa	gtgtcaacta	cagagccctc	720
tggaaccaca	gttacacagg	gaacaactcc	agagctggtg	gagaccacag	ctggagaggt	780
gtccactcct	gagcctgcgg	gttcaaatac	tagctcattc	atgcctacag	aaggtactgc	840
aggctcccctg	agtccccctgc	cggatgacac	tgccacctta	gtcctggaga	agcgccaagc	900
ccccctggat	tgtgttctgt	atcgctatgg	ctccttttcc	ctcaccctgg	acattgtcag	960
tattgagagt	gctgagatcc	tacaggctgt	gtcatccagt	gaaggagatg	catttgagct	1020
gactgtgtct	tgccaaggcg	ggctacccaa	ggaagcctgc	atggacatct	catcgccagg	1080
gtgtcagctg	cctgcccagc	ggctgtgtca	gcctgtgccc	cccagcccag	cctgccagct	1140
ggttttgcac	caggtactga	aggggtggctc	agggacctac	tgcttcaatg	tgtctttggc	1200
tgatgccaat	agcctggcga	tggtcagcac	ccagcttgtc	atgcctgggc	aagaagcagg	1260
cctcaggcag	gctcctctgt	tcgtgggcat	cctgtggtg	ctaacagctt	tgttgcttgc	1320
atctctgata	tacaggcgaa	gacttatgaa	gcaaggctca	gcagtcctcc	ttccccagct	1380
gccacacggt	agaaccagct	ggctacgtct	gccctgggtc	ttccgctctt	gccccattgg	1440
tgagagcaaa	ccccctctca	gtggacagca	ggtctgagtg	ctcttatgtg	aagtcatgat	1500
ttaccaggt	ggacagcaag	gcctgtcttt	tctctggtct	tccttcagag	actaccattg	1560
cctgaaataa	agactcagaa	cttg				1584

<210> 17  
 <211> 649  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Synthetic peptide

<400> 17

Met	Asp	Leu	Val	Leu	Arg	Lys	Tyr	Leu	Leu	His	Val	Ala	Leu	Met	Gly
1				5					10					15	

Val	Leu	Leu	Ala	Val	Arg	Thr	Thr	Glu	Gly	Pro	Arg	Asp	Arg	Asp	Trp
			20					25					30		

Leu	Gly	Val	Ser	Arg	Gln	Leu	Arg	Ile	Lys	Ala	Trp	Asn	Arg	Gln	Leu
		35					40					45			

Tyr	Pro	Glu	Trp	Thr	Glu	Ser	Gln	Gly	Pro	Asp	Cys	Trp	Arg	Gly	Gly
	50					55					60				

His	Ile	Ser	Leu	Lys	Val	Ser	Asn	Asp	Gly	Pro	Thr	Leu	Ile	Gly	Ala
65					70					75					80

Asn	Ala	Ser	Phe	Ser	Ile	Ala	Leu	His	Phe	Pro	Lys	Ser	Gln	Lys	Val
			85						90					95	

Leu	Pro	Asp	Gly	Gln	Val	Ile	Trp	Ala	Asn	Asn	Thr	Ile	Ile	Asn	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100								105							110
Ser	Gln	Val	Trp	Gly	Gly	Gln	Leu	Val	Tyr	Pro	Gln	Glu	Pro	Asp	Asp
		115					120					125			
Thr	Cys	Ile	Phe	Pro	Asp	Gly	Glu	Pro	Cys	Pro	Ser	Gly	Pro	Leu	Ser
	130					135					140				
Gln	Lys	Arg	Cys	Phe	Val	Tyr	Val	Trp	Lys	Thr	Trp	Asp	Gln	Tyr	Trp
145					150					155					160
Gln	Val	Leu	Gly	Gly	Pro	Val	Ser	Gly	Leu	Ser	Ile	Gly	Thr	Asp	Lys
				165					170					175	
Ala	Met	Leu	Gly	Thr	Tyr	Asn	Met	Glu	Val	Thr	Val	Tyr	His	Arg	Arg
			180					185					190		
Gly	Ser	Gln	Ser	Tyr	Val	Pro	Leu	Ala	His	Ser	Ser	Ser	Ala	Phe	Thr
		195					200					205			
Ile	Thr	Asp	Gln	Val	Pro	Phe	Ser	Val	Ser	Val	Ser	Gln	Leu	Gln	Ala
	210					215					220				
Leu	Asp	Gly	Arg	Asn	Lys	Arg	Phe	Leu	Arg	Lys	Gln	Pro	Leu	Thr	Phe
225					230					235					240
Ala	Leu	Gln	Leu	His	Asp	Pro	Ser	Gly	Tyr	Leu	Ala	Gly	Ala	Asp	Leu
				245					250					255	
Ser	Tyr	Thr	Trp	Asp	Phe	Gly	Asp	Ser	Thr	Gly	Thr	Leu	Ile	Ser	Arg
			260					265					270		
Ala	Leu	Thr	Val	Thr	His	Thr	Tyr	Leu	Glu	Ser	Gly	Pro	Val	Thr	Ala
		275					280					285			
Gln	Val	Val	Leu	Gln	Ala	Ala	Ile	Pro	Leu	Thr	Ser	Cys	Gly	Ser	Ser
	290					295					300				
Pro	Val	Pro	Gly	Thr	Thr	Asp	Arg	His	Val	Thr	Thr	Ala	Glu	Ala	Pro
305					310					315					320
Gly	Thr	Thr	Ala	Gly	Gln	Val	Pro	Thr	Thr	Glu	Val	Met	Gly	Thr	Thr
				325					330					335	
Pro	Gly	Gln	Val	Pro	Thr	Ala	Glu	Ala	Pro	Gly	Thr	Thr	Val	Gly	Trp
			340					345					350		

SEQCRF05081156

Val Pro Thr Thr Glu Asp Val Gly Thr Thr Pro Glu Gln Val Ala Thr  
355 360 365

Ser Lys Val Leu Ser Thr Thr Pro Val Glu Met Pro Thr Ala Lys Ala  
370 375 380

Thr Gly Arg Thr Pro Glu Val Ser Thr Thr Glu Pro Ser Gly Thr Thr  
385 390 395 400

Val Thr Gln Gly Thr Thr Pro Glu Leu Val Glu Thr Thr Ala Gly Glu  
405 410 415

Val Ser Thr Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser Phe Met Pro  
420 425 430

Thr Glu Gly Thr Ala Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala  
435 440 445

Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr  
450 455 460

Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val Gln Gly Ile Glu  
465 470 475 480

Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly Asp Ala Phe  
485 490 495

Glu Leu Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met  
500 505 510

Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu Cys Gln  
515 520 525

Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Val Leu  
530 535 540

Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Ala  
545 550 555 560

Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro Gly Gln Glu  
565 570 575

Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu Val Leu  
580 585 590

Thr Ala Leu Leu Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys  
595 600 605

SEQCRF05081156

Gln Gly Ser Ala Val Pro Leu Pro Gln Leu Pro His Gly Arg Thr Gln  
610 615 620

Trp Leu Arg Leu Pro Trp Val Phe Arg Ser Cys Pro Ile Gly Glu Ser  
625 630 635 640

Lys Pro Leu Leu Ser Gly Gln Gln Val  
645

<210> 18  
<211> 491  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Synthetic peptide

<400> 18

Gln Tyr Trp Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly  
1 5 10 15

Thr Asp Lys Ala Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr  
20 25 30

His Arg Arg Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser  
35 40 45

Ala Phe Thr Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln  
50 55 60

Leu Gln Ala Leu Asp Gly Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro  
65 70 75 80

Leu Thr Phe Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Gly  
85 90 95

Ala Asp Leu Ser Tyr Thr Trp Asp Phe Gly Asp Ser Thr Gly Thr Leu  
100 105 110

Ile Ser Arg Ala Leu Thr Val Thr His Thr Tyr Leu Glu Ser Gly Pro  
115 120 125

Val Thr Ala Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys  
130 135 140

Gly Ser Ser Pro Val Pro Gly Thr Thr Asp Arg His Val Thr Thr Ala  
145 150 155 160

SEQCRF05081156

Glu Ala Pro Gly Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Met  
165 170 175

Gly Thr Thr Pro Gly Gln Val Pro Thr Ala Glu Ala Pro Gly Thr Thr  
180 185 190

Val Gly Trp Val Pro Thr Thr Glu Asp Val Gly Thr Thr Pro Glu Gln  
195 200 205

Val Ala Thr Ser Lys Val Leu Ser Thr Thr Pro Val Glu Met Pro Thr  
210 215 220

Ala Lys Ala Thr Gly Arg Thr Pro Glu Val Ser Thr Thr Glu Pro Ser  
225 230 235 240

Gly Thr Thr Val Thr Gln Gly Thr Thr Pro Glu Leu Val Glu Thr Thr  
245 250 255

Ala Gly Glu Val Ser Thr Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser  
260 265 270

Phe Met Pro Thr Glu Gly Thr Ala Gly Ser Leu Ser Pro Leu Pro Asp  
275 280 285

Asp Thr Ala Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys  
290 295 300

Val Leu Tyr Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val Ser  
305 310 315 320

Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly Asp  
325 330 335

Ala Phe Glu Leu Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala  
340 345 350

Cys Met Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu  
355 360 365

Cys Gln Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln  
370 375 380

Val Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala  
385 390 395 400

Asp Ala Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro Gly  
405 410 415

SEQCRF05081156

Gln Glu Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu  
420 425 430

Val Leu Thr Ala Leu Leu Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu  
435 440 445

Met Lys Gln Gly Ser Ala Val Pro Leu Pro Gln Leu Pro His Gly Arg  
450 455 460

Thr Gln Trp Leu Arg Leu Pro Trp Val Phe Arg Ser Cys Pro Ile Gly  
465 470 475 480

Glu Ser Lys Pro Leu Leu Ser Gly Gln Gln Val  
485 490